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83383

From: Slobodyansky, Elizabeth  
Sent: Tuesday, December 31, 2002 12:39 PM  
To: STIC-Biotech/ChemLib  
Subject: 09/873,075

Please search for case 09/873,075:

21

SEQ ID NO: 1 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner

Art Unit 1652  
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Point of Contact:  
Mona Smith  
Technical Information Specialist  
CM1 6A01  
Tel: 308-3278

CRT

Searcher: H. Smith  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 1/2/3  
Date Completed: 1/3/5  
Searcher Prep/Review: 5  
Clerical: \_\_\_\_\_  
Online time: 4

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: 1  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

10/1/2011  
10/1/2011  
10/1/2011  
10/1/2011  
10/1/2011

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model  
Run on: January 2, 2003, 15:04:44 : Search time 15 Seconds  
(without alignments)  
380.536 Million cell updates/sec

Title: US-09-873-075A-1  
Perfect score: 999  
Sequence: 1 QLGAENGLESGSANACPDPA.....SYTIEARGEAREFLDRIRRA 194

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues  
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Issued\_Patents\_AA.\*
- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PTCTUS\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	999	100.0	229	2	US-08-817-997A-2
2	500.5	50.1	231	4	US-09-177-234-3
3	499.5	50.0	232	4	US-09-177-234-8
4	482	48.2	232	4	US-09-177-234-6
5	145	14.5	285	4	US-09-095-855-197
6	145	14.5	285	4	US-09-205-426-197
7	119	11.9	748	2	US-08-997-080-154
8	119	11.9	748	2	US-08-997-362-154
9	119	11.9	748	4	US-09-095-855-154
10	119	11.9	748	4	US-09-324-542-154
11	119	11.9	748	4	US-09-205-426-154
12	116	11.6	167	2	US-08-997-080-112
13	116	11.6	167	2	US-08-997-362-112
14	116	11.6	167	4	US-09-095-855-112
15	116	11.6	167	4	US-09-324-542-112
16	116	11.6	167	4	US-09-205-426-112
17	114.5	11.5	28	2	US-08-817-997A-3
18	90	9.0	4550	2	US-08-804-227C-8
19	90	9.0	4550	2	US-08-804-198-2
20	89	8.9	345	2	US-08-282-197C-50
21	89	8.9	592	1	US-08-217-327-8
22	86.5	8.7	200	4	US-09-355-166-18
23	76.5	7.7	1039	4	US-09-409-648-7
24	76.5	7.7	1039	4	US-09-409-648-8
25	76.5	7.7	1039	6	5196511-2
26	76	7.6	414	4	US-09-647-540A-6
27	76	7.6	428	2	US-08-657-641-6

28	76	7.6	428	5	PCT-US94-07233-6	Sequence 6, Appli
29	75.5	7.6	224	1	US-08-707-793A-6	Sequence 6, Appli
30	75.5	7.6	224	1	US-08-707-792A-6	Sequence 6, Appli
31	73.5	7.4	1056	2	US-08-627-873-7	Sequence 7, Appli
32	73	7.3	1451	1	US-08-308-872B-4	Sequence 4, Appli
33	73	7.3	1453	1	US-08-308-872B-6	Sequence 6, Appli
34	73	7.3	1454	4	US-08-392-459-22	Sequence 22, Appli
35	73	7.3	1454	4	US-08-392-459-26	Sequence 26, Appli
36	73	7.3	1454	5	PCT-US91-08525-22	Sequence 22, Appli
37	73	7.3	1454	5	PCT-US91-08525-26	Sequence 26, Appli
38	73	7.3	1454	5	PCT-US93-04384-2	Sequence 2, Appli
39	73	7.3	1454	5	PCT-US93-04384-8	Sequence 8, Appli
40	73	7.3	1454	5	PCT-US93-04384-16	Sequence 16, Appli
41	73	7.3	1454	5	PCT-US93-04384-43	Sequence 43, Appli
42	73	7.3	1454	5	PCT-US93-04384-45	Sequence 45, Appli
43	73	7.3	1454	5	PCT-US93-04384-48	Sequence 48, Appli
44	72.5	7.3	639	4	US-09-509-814A-4	Sequence 4, Appli
45	72	7.2	496	4	US-09-142-481-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-817-997A-2  
: Sequence 2, Application US/08817997A  
: Patent No. 5827719  
: GENERAL INFORMATION:  
: APPLICANT: Sandal, Thomas  
: APPLICANT: Kauppinen, Sakari  
: APPLICANT: Kofod, Lene V.  
: TITLE OF INVENTION: An Enzyme With Lipolytic  
: TITLE OF INVENTION: Activity  
: NUMBER OF SEQUENCES: 3  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: No. 58277190 No. 5827719disk Of No. 5827719th America, Inc.  
: CITY: New York  
: STATE: NY  
: COUNTRY: USA  
: ZIP: 10174  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette  
: OPERATING SYSTEM: DOS  
: SOFTWARE: FASTSEQ for Windows Version 2.0  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/817,997A  
: FILING DATE: 24-APR-1997  
: CLASSIFICATION: 7435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Landiris, Elias  
: REGISTRATION NUMBER: 33,728  
: REFERENCE/DOCKET NUMBER: 4316.204  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 212-878-9652  
: TELEFAX: 212-878-9655  
: INFORMATION FOR SEQ ID NO: 2:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 229 amino acids  
: TYPE: amino acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: FRAGMENT TYPE: internal  
US-08-817-997A-2

Query Match 100.0%; Score 999; DB 2; Length 229;  
Best Local Similarity 100.0%; Pred. NO. 9.7e-107;  
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 QLGAENGLESGSANACPDAILIFARGSTPGNMGIVGPPALANGLESIRNIWIOGVG 60  
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Db 36 QLGAIENGLESGSANACPDAILIFARGSTPEGMGTTVGPALANGLESHIRNIWIOGVGG 95
QY 61 PYDAALATNFPRTGTSQANIDEKRLFALANOKCPNTPVAVGYSOGAALIAAAVSELG 120
Db 96 PYDAALATNFPRTGTSQANIDEKRLFALANOKCPNTPVAVGYSOGAALIAAAVSELG 155
QY 121 AVKEQKGVALFGYTONLQNRGIPNPRRTKVFNCVGDVCTGTLITPAHLSYTTIEA 180
Db 156 AVKEQKGVALFGYTONLQNRGIPNPRRTKVFNCVGDVCTGTLITPAHLSYTTIEA 215
QY 181 RGEAAREFLDRDIRA 194
Db 216 RGEAAREFLDRDIRA 229

RESULT 2
US-09-177-234-3
; Sequence 3, Application US/09177234A
; Patent No. 6350604
; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Taira, Rikako
; APPLICANT: Borch, Kim
; APPLICANT: Sandal, Thomas
; APPLICANT: Halkier, Torben
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Nielsen, Bjarne R.
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; FILE REFERENCE: 4698.204-US
; CURRENT APPLICATION NUMBER: US/09/177,234A
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Gliocladium sp.
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
US-09-177-234-3

Query Match 50.1%; Score 500.5; DB 4; Length 231;
Best Local Similarity 50.0%; Pred. No. 1.8e-49;
Matches 95; Conservative 34; Mismatches 58; Indels 3; Gaps 2;

QY 5 IENGLESGSANACPDAILIFARGSTPEGMGTTVGPALANGLESHI--RNWIQGVGGPY 62
Db 42 VDELRNG-GSACPRAILIFARGTMELDNMGLLVGPALAGLEGILGSNNLWVQGVGGY 100
QY 63 DAALATNFPRTGTSQANIDEKRLFALANOKCPNTPVAVGYSOGAALIAAAVSELGAV 122
Db 101 AANLEGNLFPDGTTPKATQEMLSLLQLADTKCPNSKIIVTGGYSOGAALVAAAIRDVKASI 160
QY 123 KEQKGVALFGYTONLQNRGIPNPRRTKVFNCVGDVCTGTLITPAHLSYTTIEARG 182
Db 161 RQKIVGTVLFGYTKNKGNGQVNSTDLRYNCNAGDLICQGTLLVLPPLHLYGVQAAG 220
QY 183 EAAREFLDRDI 192
Db 221 PAAQFLASKI 230

RESULT 3
US-09-177-234-8
; Sequence 8, Application US/09177234A
; Patent No. 6350604

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; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Taira, Rikako
; APPLICANT: Borch, Kim
; APPLICANT: Sandal, Thomas
; APPLICANT: Halkier, Torben
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Nielsen, Bjarne R.
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; FILE REFERENCE: 4698.204-US
; CURRENT APPLICATION NUMBER: US/09/177,234A
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Trichophaea saccata
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
US-09-177-234-8

Query Match 50.0%; Score 499.5; DB 4; Length 232;
Best Local Similarity 50.5%; Pred. No. 2.3e-49;
Matches 96; Conservative 32; Mismatches 59; Indels 3; Gaps 2;

QY 5 IENGLESGSANACPDAILIFARGSTPEGMGTTVGPALANGLESHI--RNWIQGVGGPY 62
Db 42 VDELRNG-GGACPRAILIFARGTMELDNMGLLVGPALAGLEGILGSNNLWVQGVGGY 100
QY 63 DAALATNFPRTGTSQANIDEKRLFALANOKCPNTPVAVGYSOGAALIAAAVSELGAV 122
Db 101 AANLEGNLFPDGTTPKATQEMLSLLQLADTKCPNSKIIVTGGYSOGAALVAAAIRDVKASI 160
QY 123 KEQKGVALFGYTONLQNRGIPNPRRTKVFNCVGDVCTGTLITPAHLSYTTIEARG 182
Db 161 RQKIVGTVLFGYTKNKGNGQVNSTDLRYNCNAGDLICQGTLLVLPPLHLYGVQAAG 220
QY 183 EAAREFLDRDI 192
Db 221 PAAQFLASKI 230

RESULT 4
US-09-177-234-6
; Sequence 6, Application US/09177234A
; Patent No. 6350604
; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Taira, Rikako
; APPLICANT: Borch, Kim
; APPLICANT: Sandal, Thomas
; APPLICANT: Halkier, Torben
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Nielsen, Bjarne R.
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; FILE REFERENCE: 4698.204-US
; CURRENT APPLICATION NUMBER: US/09/177,234A
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8

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SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 6

LENGTH: 232

TYPE: PRT

ORGANISM: Verticillium sp.

FEATURE:

NAME/KEY: SIGNAL

LOCATION: (1)...(30)

US-09-177-234-6

Query Match 48.2%; Score 482; DB 4; Length 232;

Best Local Similarity 49.7%; Pred. No. 2.4e-47;

Matches 90; Conservative 33; Mismatches 56; Indels 2; Gaps 1;

QY 16 ACPDAILIFARGSTFGNMGITVGPALANGLESHT--RNIIWIOGVGPPYDAALATNPLR 73

DB 52 ACPKALIFARGTIELDNGLVGPLADGLSGILGSKNLWVGVGQVAASLEGNLFDP 111

QY 74 GTSQANIDEGKRLFALANOKPNTVPVAGYSOGAALIAAVALSELGAVKEQVKGVALFG 133

DB 112 GTPPQAIQEMITLQLADTKCPNSKIVTGGYSOGAALVAAAIIRDVKASIRKQIVGTVLFG 171

QY 134 YTNLQNRGIGPNVPRRTKVFNCVGDVCTGTLITPAHLSYTIIEARGEAREFLRDRIR 193

DB 172 YSNKORNGQVENYSNDRLRVYCNPGDLICEGTLIPLVHLLYGNQAGSPAAQFLASKIN 231

QY 194 A 194

DB 232 S 232

RESULT 5

US-09-095-855-197

Sequence 197, Application US/09095855

Patent No. 6160093

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: Compounds and Methods for Mycobacterial Infections

TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections

NUMBER OF SEQUENCES: 208

CORRESPONDENCE ADDRES:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,855

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,347

FILING DATE: 29-AUG-1996

APPLICATION NUMBER: 08/873,970

FILING DATE: 12-JUN-1997

APPLICATION NUMBER: 08/997,362

FILING DATE: 23-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 197:

SEQUENCE CHARACTERISTICS:

LENGTH: 285 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-095-855-197

Query Match

Best Local Similarity 14.5%; Score 145; DB 4; Length 285;

Matches 60; Conservative 31; Mismatches 71; Indels 48; Gaps 14;

QY 9 LESGSANACPDAILIFARGSTFGNMGITVGPALANGLESHTRNIIWIOGVGPPYDAALA 67

DB 27 IPTASADPCPDIEVIFARGTGAEPG-LG-WVGDAFVNALRPKVG-----QSVG-----TYA 76

QY 68 TNP-----LPRGTSQANIDEGKRLFALANOKPNTVPVAGYSOGAALIAAAV--- 115

DB 77 VNPAGFDFDKSAPMGAAADAS---GRVQWMADN--CPDTKLVLGMSQAGVIDLITVDP 131

QY 116 -----SELGAVKEQVKGVALFGY-TQNLRNGRIGIPNYP---RERTKVFNCVGDVAVC 163

DB 132 RPLGRFTPTMPPRVADHVAAYVVFVGNPLRDIRGGPLPQMSTGYGPKSIDLCALDDPFC 191

QY 164 TGTLLITPAHLSYTI-----TEARGEAAARFLR 189

DB 192 SPGFNL-PAHFAYADNGWVE---EAAANFAR 217

RESULT 6

US-09-205-426-197

Sequence 197, Application US/09205426

Patent No. 6406704

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L. J.

TITLE OF INVENTION: Compounds and Methods for Treatment and

TITLE OF INVENTION: Diagnosis of Mycobacterial Infections

FILE REFERENCE: 11000.1002c4

CURRENT APPLICATION NUMBER: US/09/205,426

CURRENT FILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: 09/095,855

EARLIER FILING DATE: 1998-06-11

EARLIER APPLICATION NUMBER: 08/997,362

EARLIER FILING DATE: 1997-12-23

EARLIER APPLICATION NUMBER: 08/873,970

EARLIER FILING DATE: 1997-06-12

EARLIER APPLICATION NUMBER: 08/705,347

EARLIER FILING DATE: 1996-08-29

NUMBER OF SEQ ID NOS: 208

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 197

LENGTH: 285

TYPE: PRT

ORGANISM: Mycobacterium vaccae

US-09-205-426-197

Query Match

Best Local Similarity 14.5%; Score 145; DB 4; Length 285;

Matches 60; Conservative 31; Mismatches 71; Indels 48; Gaps 14;

QY 9 LESGSANACPDAILIFARGSTFGNMGITVGPALANGLESHTRNIIWIOGVGPPYDAALA 67

DB 27 IPTASADPCPDIEVIFARGTGAEPG-LG-WVGDAFVNALRPKVG-----QSVG-----TYA 76

QY 68 TNP-----LPRGTSQANIDEGKRLFALANOKPNTVPVAGYSOGAALIAAAV--- 115

DB 77 VNPAGFDFDKSAPMGAAADAS---GRVQWMADN--CPDTKLVLGMSQAGVIDLITVDP 131

QY 116 -----SELGAVKEQVKGVALFGY-TQNLRNGRIGIPNYP---RERTKVFNCVGDVAVC 163

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Db 132 RPLGRFTPTMPRVADHVAVVVFNPLRDIRGGPLQMSGTYPKPSIDICALDDPFC 191
Qy 164 TCTLIITPAHLSYT---IEARGEARFLR 189
Db 192 SPGFNL-PAHFAYADNGWVE---EARNFAR 217

RESULT 7
US-08-997-080-154
; Sequence 154, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 748 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-997-080-154

Query Match 11.9%; Score 119; DB 2; Length 748;
Best Local Similarity 31.1%; Pred. No. 6.7e-05;
Matches 51; Conservative 21; Mismatches 52; Indels 40; Gaps 12;

Qy 9 LESGSANACPDAILIFARG-S-TEPGNMGITVGPALANGLESIRNIWTQGVGPDAAALA 67
Db 27 IPTASADPCPDIEVIFARGTGAEPG-LG-WVGDAFVNALRPKVG----QSVG-----TYA 76

Qy 68 TNF-----LPRGTQANIDEGKRLFALANQKCPNTVPVAGGYSOGAALIAAAV--- 115
Db 77 VNPAGFDKSPAPMGAAAS----GRVQWMDN--CPDTKLVLGMSXGAGVIDLITVDP 131

Qy 116 -----SELGAVKEQVKGVLFQYTNQLN--RGGIPNY-PR 149
Db 132 RPLGRFTPTMPRVADHVAVVVFG--NPLRDIRGGGPRLEPR 173

RESULT 8
US-08-997-362-154
; Sequence 154, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
```

```
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 748 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-997-362-154

Query Match 11.9%; Score 119; DB 2; Length 748;
Best Local Similarity 31.1%; Pred. No. 6.7e-05;
Matches 51; Conservative 21; Mismatches 52; Indels 40; Gaps 12;

Qy 9 LESGSANACPDAILIFARG-S-TEPGNMGITVGPALANGLESIRNIWTQGVGPDAAALA 67
Db 27 IPTASADPCPDIEVIFARGTGAEPG-LG-WVGDAFVNALRPKVG----QSVG-----TYA 76

Qy 68 TNF-----LPRGTQANIDEGKRLFALANQKCPNTVPVAGGYSOGAALIAAAV--- 115
Db 77 VNPAGFDKSPAPMGAAAS----GRVQWMDN--CPDTKLVLGMSXGAGVIDLITVDP 131

Qy 116 -----SELGAVKEQVKGVLFQYTNQLN--RGGIPNY-PR 149
Db 132 RPLGRFTPTMPRVADHVAVVVFG--NPLRDIRGGGPRLEPR 173

RESULT 9
US-09-095-855-154
; Sequence 154, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
```



Db 132 RPLGRFTPTMPPRVADHVAHVVFVFG--NPLRDIRGGPRLEPR 173

RESULT 12

US-08-997-080-112  
; Sequence 112, Application US/08997080  
; Patent No. 5968524  
; GENERAL INFORMATION:  
; APPLICANT: WATSON, JAMES D.  
; APPLICANT: TAN, PAUL L.J.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-  
; NUMBER OF SEQUENCES: 194  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/997,080  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sleath, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000.1007  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; TELEX:

INFORMATION FOR SEQ ID NO: 112:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 167 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-997-080-112

Query Match 11.6%; Score 116; DB 2; Length 167;  
Best Local Similarity 30.1%; Pred. No. 1.6e-05;  
Matches 44; Conservative 19; Mismatches 47; Indels 36; Gaps 9;  
QY 9 LESSGANACPDAILIFARGSG-TEPCNMGITVGPALANGLESHIRNIWIGVGGPYDAALA 67  
Db 27 IPTASADPCDIEVIFARGTGAEPG-LG-WGDAFVNALRPKVG----QSVG-----TYA 76  
QY 68 TNF-----LPRGTSQANIDEGRKLFALANQCPNTPVVGYSOGAALIAAAV--- 115  
Db 77 VNYPAAGDFDKSAPMGAAADAS---GRVQWMDN--CPDTKLVLGMSXGAGVIDLITVDP 131  
QY 116 -----SELGAVKEQVKGVALFG 133  
Db 132 RPLGRFTPTMPPRVADHVAHVVFVFG 157

RESULT 13

US-08-997-362-112  
; Sequence 112, Application US/08997362  
; Patent No. 5985287  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Paul  
; APPLICANT: Hiyama, Jun  
; APPLICANT: Visser, Elizabeth

; APPLICANT: Skinner, Margot  
; APPLICANT: Scott, Linda  
; APPLICANT: Prestidge, Ross  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS  
; NUMBER OF SEQUENCES: 194  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/997,362  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970  
; FILING DATE: June 12, 1997  
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347  
; FILING DATE: August 29, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sleath, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000.1002c2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; TELEX:

INFORMATION FOR SEQ ID NO: 112:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 167 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-997-362-112

Query Match 11.6%; Score 116; DB 2; Length 167;  
Best Local Similarity 30.1%; Pred. No. 1.6e-05;  
Matches 44; Conservative 19; Mismatches 47; Indels 36; Gaps 9;  
QY 9 LESSGANACPDAILIFARGSG-TEPCNMGITVGPALANGLESHIRNIWIGVGGPYDAALA 67  
Db 27 IPTASADPCDIEVIFARGTGAEPG-LG-WGDAFVNALRPKVG----QSVG-----TYA 76  
QY 68 TNF-----LPRGTSQANIDEGRKLFALANQCPNTPVVGYSOGAALIAAAV--- 115  
Db 77 VNYPAAGDFDKSAPMGAAADAS---GRVQWMDN--CPDTKLVLGMSXGAGVIDLITVDP 131  
QY 116 -----SELGAVKEQVKGVALFG 133  
Db 132 RPLGRFTPTMPPRVADHVAHVVFVFG 157

RESULT 14

US-09-095-855-112  
; Sequence 112, Application US/09095855  
; Patent No. 6160093  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Paul  
; APPLICANT: Visser, Elizabeth  
; APPLICANT: Skinner, Margot  
; APPLICANT: Prestidge, Ross  
; TITLE OF INVENTION: Compounds and Methods for  
; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections  
; NUMBER OF SEQUENCES: 208

US-09-095-855-112  
; Sequence 112, Application US/09095855  
; Patent No. 6160093  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Paul  
; APPLICANT: Visser, Elizabeth  
; APPLICANT: Skinner, Margot  
; APPLICANT: Prestidge, Ross  
; TITLE OF INVENTION: Compounds and Methods for  
; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections  
; NUMBER OF SEQUENCES: 208



;; EARLIER FILING DATE: 1997  
; NUMBER OF SEQ ID NOS: 194

[illegible]

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RESULT 15
US-09-324-542-112
; Sequence 112, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 2, 2003, 15:01:13 ; Search time 36 seconds  
(without alignments)  
718.073 Million cell updates/sec

Title: US-09-873-075a-1  
Perfect score: 999  
Sequence: 1 QLCATENGLESGSANACPD.....SYTIEARGEARFLDRIR 194

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	996	99.7	194	21	AA13715
3	995	99.6	194	21	AA13706
4	995	99.6	194	23	AB176837
5	995	99.6	194	23	AB176838
6	995	99.6	194	23	AB176844
7	993	99.4	194	21	AA13707
8	993	99.4	194	23	AB176839
9	992	99.3	194	21	AA13703
10	991	99.2	194	21	AA13704

11	991	99.2	194	23	AB176845	Mutant Humicola in
12	991	99.2	246	17	AA195051	H. insolens lipase
13	990	99.1	194	21	AA13705	H. insolens mutant
14	990	99.1	194	21	AA13711	H. insolens mutant
15	990	99.1	194	23	AB176829	Mutant Humicola in
16	989	99.0	194	21	AA13710	H. insolens mutant
17	989	99.0	194	23	AB176834	Mutant Humicola in
18	988	98.9	194	23	AB176831	Mutant Humicola in
19	987	98.8	194	21	AA13717	H. insolens mutant
20	985	98.6	194	21	AA13716	H. insolens mutant
21	984	98.5	194	21	AA13709	H. insolens mutant
22	984	98.5	194	23	AB176830	Mutant Humicola in
23	983	98.4	194	23	AB176836	Mutant Humicola in
24	983	98.4	194	23	AB176843	Mutant Humicola in
25	983	98.4	194	23	AB176846	Mutant Humicola in
26	982	98.3	194	21	AA13708	H. insolens mutant
27	978	97.9	194	23	AB176828	Mutant Humicola in
28	978	97.9	194	23	AB176832	Mutant Humicola in
29	977	97.8	194	21	AA13718	H. insolens mutant
30	977	97.8	194	23	AB176857	Mutant Humicola in
31	976	97.7	194	23	AB176827	Mutant Humicola in
32	976	97.7	194	23	AB176835	Mutant Humicola in
33	974	97.5	194	21	AA13719	H. insolens mutant
34	973	97.4	194	23	AB176833	Mutant Humicola in
35	971	97.2	194	21	AA13712	H. insolens mutant
36	971	97.2	194	21	AA13714	H. insolens mutant
37	969	97.0	194	23	AB176841	Mutant Humicola in
38	965	96.6	194	21	AA13713	H. insolens mutant
39	960	96.1	194	23	AB176847	Mutant Humicola in
40	955	95.6	194	23	AB176840	Mutant Humicola in
41	955	95.6	194	23	AB176851	Mutant Humicola in
42	954	95.5	194	23	AB176848	Mutant Humicola in
43	954	95.5	194	23	AB176849	Mutant Humicola in
44	954	95.5	194	23	AB176850	Mutant Humicola in
45	953	95.4	194	23	AB176855	Mutant Humicola in

ALIGNMENTS

RESULT 1  
AA198435  
ID AA198435 standard; protein; 194 AA.  
AC  
AA198435;  
XX  
XX  
DT 25-JUN-2002 (first entry)  
XX  
XX Wild-type Humicola insolens mature cutinase.  
DE  
DE Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin.  
KW  
KW Humicola insolens strain DSM 1800.  
XX  
XX WO200192502-A1.  
XX  
XX 06-DEC-2001.  
XX  
XX 22-MAY-2001; 2001WO-DK00350.  
XX  
XX 02-JUN-2000; 2000DK-0000861.  
PR 23-OCT-2000; 2000DK-0001577.  
PR 24-NOV-2000; 2000DK-0001772.  
PR 19-JAN-2001; 2001DK-0000100.  
XX  
XX (NOVO ) NOVOZYMES AS.  
PA Svendsen A, Glad SOS, Fukuyama S, Matsui T;  
XX WPI; 2002-216714/27.  
XX Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic  
PT oligomers of poly(ethylene terephthalate), comprises a substitution of

PT amino acid residues corresponding to positions of Humicola insolens  
 PT cutinase -  
 XX  
 XX Disclosure; Page 36; 4lpp; English.  
 XX  
 CC The present sequence is the wild-type mature cutinase from Humicola  
 CC insolens strain DSM 1800, which was used to generate mutant cutinases  
 CC (see ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic enzymes  
 CC capable of hydrolysing the substrate cutin. The mutant cutinases have  
 CC improved thermostability, and are used for enzymatic hydrolysis  
 CC of cyclic oligomers of poly(ethylene terephthalate), e.g. in the  
 CC finishing of yarn or fabric from poly(ethylene terephthalate) fibers.  
 XX  
 XX Sequence 194 AA;  
 SQ  
 Query Match 100.0%; Score 999; DB 23; Length 194;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-100;  
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QLGAIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWQGVGG 60  
 DB 1 QLGAIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWQGVGG 60  
 QY 61 PYDAALATNLFPRGTSQANIDEGKRLFALANOKCPNTPVAVGGYSGGAALIAAAVSELGG 120  
 DB 61 PYDAALATNLFPRGTSQANIDEGKRLFALANOKCPNTPVAVGGYSGGAALIAAAVSELGG 120  
 QY 121 AVKEQKGVALLFGYTONLQNRGGIPNYPRTKVKFCNVGDVCTGLTIITPAHLSYTTIEA 180  
 DB 121 AVKEQKGVALLFGYTONLQNRGGIPNYPRTKVKFCNVGDVCTGLTIITPAHLSYTTIEA 180  
 QY 181 RGEAARFLDRIRA 194  
 DB 181 RGEAARFLDRIRA 194  
 RESULT 2  
 AAB13715  
 ID AAB13715 standard; Protein; 194 AA.  
 XX  
 AC AAB13715;  
 DT 17-NOV-2000 (first entry)  
 XX  
 DE H. insolens mutant cutinase, E1790 substitution.  
 XX  
 KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;  
 KW thermostability; enzyme; lipolytic; fabric finishing; yarn;  
 KW protein co-ordinate.  
 XX  
 OS Humicola insolens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 179  
 FT /note= "Wild-type Glu substituted by Gln"  
 XX  
 PN WO200034450-A1.  
 XX  
 XX 15-JUN-2000.  
 XX  
 XX 03-DEC-1999; 99WO-DK00678.  
 XX  
 PR 04-DEC-1998; 98DK-0001604.  
 PR 09-DEC-1998; 98US-0111591.  
 PR 09-MAR-1999; 99DK-0000330.  
 PR 16-MAR-1999; 99US-0124671.  
 XX  
 XX (NOVO ) NOVO-NORDISK AS.  
 FA  
 XX Abo M, Fukuyama S, Svendsen A, Matsui T;  
 PI WPI; 2000-482424/42.  
 XX  
 DR

XX Thermostable variant of parent fungal cutinase useful for dyeing  
 PT polyester yarn or fabric, comprises substitution of amino acid residues  
 PT at predetermined positions from the N-terminal amino acid -  
 XX  
 XX Example 1; Page -; 79pp; English.  
 PS  
 XX Site-directed mutagenesis was carried out on wild-type Humicola insolens  
 CC cutinase, to produce the present sequence. The introduced substitution  
 CC improves the thermostability of the cutinase enzyme. Cutinases are  
 CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase  
 CC may be used in the enzymatic hydrolysis of cyclic oligomers of  
 CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from  
 CC poly(ethylene terephthalate) fibers. Cutinase variants with improved  
 CC thermostability are useful since they can withstand higher processing  
 CC temperatures.  
 CC Note: the present sequence is not shown in the specification but is  
 CC derived from the H. insolens wild-type cutinase sequence given in SEQ ID  
 CC 2 of patent: US 5,827,719.  
 XX  
 SQ Sequence 194 AA;  
 Query Match 99.7%; Score 996; DB 21; Length 194;  
 Best Local Similarity 99.5%; Pred. No. 7.2e-100;  
 Matches 193; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QLGAIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWQGVGG 60  
 DB 1 QLGAIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWQGVGG 60  
 QY 61 PYDAALATNLFPRGTSQANIDEGKRLFALANOKCPNTPVAVGGYSGGAALIAAAVSELGG 120  
 DB 61 PYDAALATNLFPRGTSQANIDEGKRLFALANOKCPNTPVAVGGYSGGAALIAAAVSELGG 120  
 QY 121 AVKEQKGVALLFGYTONLQNRGGIPNYPRTKVKFCNVGDVCTGLTIITPAHLSYTTIEA 180  
 DB 121 AVKEQKGVALLFGYTONLQNRGGIPNYPRTKVKFCNVGDVCTGLTIITPAHLSYTTIEA 180  
 QY 181 RGEAARFLDRIRA 194  
 DB 181 RGEAARFLDRIRA 194  
 RESULT 3  
 AAB13706  
 ID AAB13706 standard; Protein; 194 AA.  
 XX  
 AC AAB13706;  
 XX  
 DT 17-NOV-2000 (first entry)  
 XX  
 DE H. insolens mutant cutinase, E47K substitution.  
 XX  
 KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;  
 KW thermostability; enzyme; lipolytic; fabric finishing; yarn;  
 KW protein co-ordinate.  
 XX  
 OS Humicola insolens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 47  
 FT /note= "Wild-type Glu substituted by Lys"  
 XX  
 PN WO200034450-A1.  
 XX  
 XX 15-JUN-2000.  
 XX  
 XX 03-DEC-1999; 99WO-DK00678.  
 XX  
 PR 04-DEC-1998; 98DK-0001604.  
 PR 09-DEC-1998; 98US-0111591.  
 PR 09-MAR-1999; 99DK-0000330.  
 PR

PR 16-MAR-1999; 99US-0124671.  
XX (NOVO ) NOVO-NORDISK AS.  
PA Abo M, Fukuyama S, Svendsen A, Matsui T;  
PI WPI; 2000-482424/42.  
XX Thermostable variant of parent fungal cutinase useful for dyeing  
PT polyester yarn or fabric, comprises substitution of amino acid residues  
PT at predetermined positions from the N-terminal amino acid -  
XX  
XX  
PS Claim 15; Page -: 79pp; English.  
XX  
XX Site-directed mutagenesis was carried out on wild-type Humicola insolens  
CC cutinase, to produce the present sequence. The introduced substitution  
CC improves the thermostability of the cutinase enzyme. Cutinases are  
CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase  
CC may be used in the enzymatic hydrolysis of cyclic oligomers of  
CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from  
CC poly(ethylene terephthalate) fibers. Cutinase variants with improved  
CC thermostability are useful since they can withstand higher processing  
CC temperatures.  
CC Note: the present sequence is not shown in the specification but is  
CC derived from the H. insolens wild-type cutinase sequence given in SEQ ID  
CC 2 of patent: US 5,827,719.  
XX  
XX Sequence 194 AA;  
SQ  
Query Match 99.6%; Score 995; DB 21; Length 194;  
Best Local Similarity 99.5%; Pred. No. 9.3e-100;  
Matches 193; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGLESIRNIWIOGVG 60  
DB 1 QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGLESIRNIWIOGVG 60  
QY 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVVAGYSOGAALIAAAVSELG 120  
DB 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVVAGYSOGAALIAAAVSELG 120  
QY 121 AVKEQVKGVALFGYTONLQNRGIPNYPRTKVFNCVGDVCTGTLITPAHLSTTIEA 180  
DB 121 AVKEQVKGVALFGYTONLQNRGIPNYPRTKVFNCVGDVCTGTLITPAHLSTTIEA 180  
QY 181 RGEAARFLDRIRA 194  
DB 181 RGEAARFLDRIRA 194  
RESULT 4  
ABB76837  
XX ABB76837 standard; Protein; 194 AA.  
XX ABB76837;  
XX 25-JUN-2002 (first entry)  
XX Mutant Humicola insolens mature cutinase #11.  
XX  
XX Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.  
XX  
XX Humicola insolens strain DSM 1800.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 164  
FT /note= "Wild-type Thr substituted by Ser"  
XX  
XX WO200192502-A1.  
XX  
XX 06-DEC-2001.  
XX

PF 22-MAY-2001; 2001WO-DK00350.  
XX  
XX 02-JUN-2000; 2000DK-0000861.  
PR 23-OCT-2000; 2000DK-0001577.  
PR 24-NOV-2000; 2000DK-0001772.  
PR 19-JAN-2001; 2001DK-0000100.  
XX  
XX (NOVO ) NOVOZYMES AS.  
PA  
XX Svendsen A, Glad SOS, Fukuyama S, Matsui T;  
PI WPI; 2002-216714/27.  
XX  
XX Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic  
PT oligomers of poly(ethylene terephthalate), comprises a substitution of  
PT amino acid residues corresponding to positions of Humicola insolens  
PT cutinase -  
XX  
XX Claim 8; Page -: 41pp; English.  
XX  
XX The present invention relates to wild-type mature cutinase from Humicola  
CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant  
CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic  
CC enzymes capable of hydrolysing the substrate cutin. The mutant cutinases  
CC have improved thermostability, and are used for enzymatic hydrolysis  
CC of cyclic oligomers of poly(ethylene terephthalate), e.g. in the  
CC finishing of yarn or fabric from poly(ethylene terephthalate) fibers.  
CC Note: the present sequence is not shown in the specification, but is  
CC derived from the wild-type cutinase sequence shown on page 36.  
XX  
XX Sequence 194 AA;  
SQ  
Query Match 99.6%; Score 995; DB 23; Length 194;  
Best Local Similarity 99.5%; Pred. No. 9.3e-100;  
Matches 193; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGLESIRNIWIOGVG 60  
DB 1 QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGLESIRNIWIOGVG 60  
QY 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVVAGYSOGAALIAAAVSELG 120  
DB 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVVAGYSOGAALIAAAVSELG 120  
QY 121 AVKEQVKGVALFGYTONLQNRGIPNYPRTKVFNCVGDVCTGTLITPAHLSTTIEA 180  
DB 121 AVKEQVKGVALFGYTONLQNRGIPNYPRTKVFNCVGDVCTGTLITPAHLSTTIEA 180  
QY 181 RGEAARFLDRIRA 194  
DB 181 RGEAARFLDRIRA 194  
RESULT 5  
ABB76838  
XX ABB76838 standard; Protein; 194 AA.  
XX ABB76838;  
XX  
XX 25-JUN-2002 (first entry)  
XX  
XX Mutant Humicola insolens mature cutinase #12.  
XX  
XX Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.  
XX  
XX Humicola insolens strain DSM 1800.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 174  
FT /note= "Wild-type Leu substituted by Phe"  
XX  
XX WO200192502-A1.

```

XX PD 06-DEC-2001.
XX PF 22-MAY-2001; 2001WO-DK00350.
XX PR 02-JUN-2000; 2000DK-0000861.
XX PR 23-OCT-2000; 2000DK-0001577.
XX PR 24-NOV-2000; 2000DK-0001772.
XX PR 19-JAN-2001; 2001DK-0000100.
XX PA (NOVO ) NOVOZYMES AS.
XX PI Svendsen A, Glad SOS, Fukuyama S, Matsui T;
XX DR WPI; 2002-216714/27.
XX PT Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
XX PT oligomers of poly(ethylene terephthalate), comprises a substitution of
XX PT amino acid residues corresponding to positions of Humicola insolens
XX PS cutinase -
XX PS Claim 8; Page -: 41pp; English.
XX CC The present invention relates to wild-type mature cutinase from Humicola
XX CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant
XX CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic
XX CC enzymes capable of hydrolysing the substrate cutin. The mutant cutinases
XX CC have improved thermostability, and are used for enzymatic hydrolysis
XX CC of cyclic oligomers of poly(ethylene terephthalate), e.g. in the
XX CC finishing of yarn or fabric from poly(ethylene terephthalate) fibers.
XX CC Note: the present sequence in not shown in the specification, but is
XX CC derived from the wild-type cutinase sequence shown on page 36.
XX SQ Sequence 194 AA;

Query Match 99.6%; Score 995; DB 23; Length 194;
Best Local Similarity 99.5%; Pred. No. 9.3e-100;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLGAIENGLESGSNACPDAILIFARGSTPEGNMGITVGPALANGLESHIRNIWQVGG 60
Db 1 QLGAIENGLESGSNACPDAILIFARGSTPEGNMGITVGPALANGLESHIRNIWQVGG 60

Qy 61 PYDAALATNFTLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
Db 61 PYDAALATNFTLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120

Qy 121 AVKEQVKGVALLFGYTONLQNRGGIPNYPRTKVFNCVGDVAVCTGLTIITPAHLSYITIEA 180
Db 121 AVKEQVKGVALLFGYTONLQNRGGIPNYPRTKVFNCVGDVAVCTGLTIITPAHLSYITIEA 180

Qy 181 RGEAARFLDRIRA 194
Db 181 RGEAARFLDRIRA 194

RESULT 6
ABB76844
ID ABB76844 standard; Protein; 194 AA.
XX AC ABB76844;
XX AC ABB76844;
XX DT 25-JUN-2002 (first entry)
XX DE Mutant Humicola insolens mature cutinase #18.
XX KW Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
XX OS Humicola insolens strain DSM 1800.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 130

```

```

FT XX /note= "Wild-type Arg substituted by Val"
PN XX WO200192502-A1.
XX PD 06-DEC-2001.
XX PF 22-MAY-2001; 2001WO-DK00350.
XX PR 02-JUN-2000; 2000DK-0000861.
XX PR 23-OCT-2000; 2000DK-0001577.
XX PR 24-NOV-2000; 2000DK-0001772.
XX PR 19-JAN-2001; 2001DK-0000100.
XX PA (NOVO ) NOVOZYMES AS.
XX PI Svendsen A, Glad SOS, Fukuyama S, Matsui T;
XX DR WPI; 2002-216714/27.
XX PT Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
XX PT oligomers of poly(ethylene terephthalate), comprises a substitution of
XX PT amino acid residues corresponding to positions of Humicola insolens
XX PS cutinase -
XX PS Claim 8; Page -: 41pp; English.
XX CC The present invention relates to wild-type mature cutinase from Humicola
XX CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant
XX CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic
XX CC enzymes capable of hydrolysing the substrate cutin. The mutant cutinases
XX CC have improved thermostability, and are used for enzymatic hydrolysis
XX CC of cyclic oligomers of poly(ethylene terephthalate), e.g. in the
XX CC finishing of yarn or fabric from poly(ethylene terephthalate) fibers.
XX CC Note: the present sequence in not shown in the specification, but is
XX CC derived from the wild-type cutinase sequence shown on page 36.
XX SQ Sequence 194 AA;

Query Match 99.6%; Score 995; DB 23; Length 194;
Best Local Similarity 99.5%; Pred. No. 9.3e-100;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QLGAIENGLESGSNACPDAILIFARGSTPEGNMGITVGPALANGLESHIRNIWQVGG 60
Db 1 QLGAIENGLESGSNACPDAILIFARGSTPEGNMGITVGPALANGLESHIRNIWQVGG 60

Qy 61 PYDAALATNFTLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
Db 61 PYDAALATNFTLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120

Qy 121 AVKEQVKGVALLFGYTONLQNRGGIPNYPRTKVFNCVGDVAVCTGLTIITPAHLSYITIEA 180
Db 121 AVKEQVKGVALLFGYTONLQNRGGIPNYPRTKVFNCVGDVAVCTGLTIITPAHLSYITIEA 180

Qy 181 RGEAARFLDRIRA 194
Db 181 RGEAARFLDRIRA 194

RESULT 7
AAB13707
ID AAB13707 standard; Protein; 194 AA.
XX AC AAB13707;
XX AC AAB13707;
XX DT 17-NOV-2000 (first entry)
XX DE H. insolens mutant cutinase, E179X substitution.
XX KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;
XX KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
XX KW protein co-ordinate.

```

OS Humicola insolens.  
XX Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1/9 /note= "wild-type Glu substituted by Asn or Gln"  
XX  
XX  
XX W0200034450-A1.  
XX  
XX 15-JUN-2000.  
XX  
XX 03-DEC-1999; 99WO-DK00678.  
XX  
XX 04-DEC-1998; 98DK-0001604.  
PR 09-DEC-1998; 98US-0111591.  
PR 09-MAR-1999; 99DK-0000330.  
PR 16-MAR-1999; 99US-0124671.  
XX  
XX (NOVO ) NOVO-NORDISK AS.  
XX  
XX Abo M., Fukuyama S., Svendsen A., Matsui T;  
XX  
XX WPI; 2000-482424/42.  
XX  
XX Thermostable variant of parent fungal cutinase useful for dyeing  
PT polyester yarn or fabric, comprises substitution of amino acid residues  
PT at predetermined positions from the N-terminal amino acid  
XX  
XX Claim 16; Page -: 79pp; English.  
XX  
XX Site-directed mutagenesis was carried out on wild-type Humicola insolens  
CC cutinase, to produce the present sequence. The introduced substitution  
CC improves the thermostability of the cutinase enzyme. Cutinases are  
CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase  
CC may be used in the enzymatic hydrolysis of cyclic oligomers of  
CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from  
CC poly(ethylene terephthalate) fibers. Cutinase variants with improved  
CC thermostability are useful since they can withstand higher processing  
CC temperatures.  
CC Note: the present sequence is not shown in the specification but is  
CC derived from the H. insolens wild-type cutinase sequence given in SEQ ID  
CC 2 of patent: US 5,827,719.  
XX  
XX Sequence 194-AA;  
SQ  
Query Match 99.4%; Score 993; DB 21; Length 194;  
Best Local Similarity 99.5%; Pred. No. 1.5e-99;  
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHTIRNIWIOGVG 60  
DB 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHTIRNIWIOGVG 60  
QY 61 PYDAALATNPLRGTSQANIDEKRLFALANQKCPNTPPVAGGYSOGAALIAAAVSELG 120  
DB 61 PYDAALATNPLRGTSQANIDEKRLFALANQKCPNTPPVAGGYSOGAALIAAAVSELG 120  
QY 121 AVKEQKGVAGLFGYTONLQNRGGIPNYPRTKVFNCVNGDAVCTGLTIITPAHLSVTIEA 180  
DB 121 AVKEQKGVAGLFGYTONLQNRGGIPNYPRTKVFNCVNGDAVCTGLTIITPAHLSVTIEA 180  
QY 181 RGEAARFLDRIRA 194  
DB 181 RGEAARFLDRIRA 194  
RESULT 8  
ABB76839  
ID ABB76839 standard; Protein; 194 AA.  
XX  
AC ABB76839;  
XX  
DT 25-JUN-2002 (first entry)

XX Mutant Humicola insolens mature cutinase #13.  
XX  
XX Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.  
XX  
XX Humicola insolens strain DSM 1800.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 49 /note= "wild-type His substituted by Tyr"  
FT  
XX  
XX W0200192502-A1.  
XX  
XX 06-DEC-2001.  
XX  
XX 22-MAY-2001; 2001WO-DK00350.  
XX  
XX 02-JUN-2000; 2000DK-0000861.  
PR 23-OCT-2000; 2000DK-0001577.  
PR 24-NOV-2000; 2000DK-0001772.  
PR 19-JAN-2001; 2001DK-0000100.  
XX  
XX (NOVO ) NOVOZYMES AS.  
XX  
XX Svendsen A., Glad SOS, Fukuyama S., Matsui T;  
XX  
XX WPI; 2002-216714/27.  
XX  
XX Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic  
PT oligomers of poly(ethylene terephthalate), comprises a substitution of  
PT amino acid residues corresponding to positions of Humicola insolens  
PT cutinase -  
XX  
XX Claim 8; Page -: 41pp; English.  
XX  
XX The present invention relates to wild-type mature cutinase from Humicola  
CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant  
CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic  
CC enzymes capable of hydrolysing the substrate cutin. The mutant cutinases  
CC have improved thermostability, and are used for enzymatic hydrolysis  
CC of cyclic oligomers of poly(ethylene terephthalate), e.g. in the  
CC finishing of yarn or fabric from poly(ethylene terephthalate) fibers.  
CC Note: the present sequence in not shown in the specification, but is  
CC derived from the wild-type cutinase sequence shown on page 36.  
XX  
XX Sequence 194 AA;  
SQ  
Query Match 99.4%; Score 993; DB 23; Length 194;  
Best Local Similarity 99.5%; Pred. No. 1.5e-99;  
Matches 193; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHTIRNIWIOGVG 60  
DB 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHTIRNIWIOGVG 60  
QY 61 PYDAALATNPLRGTSQANIDEKRLFALANQKCPNTPPVAGGYSOGAALIAAAVSELG 120  
DB 61 PYDAALATNPLRGTSQANIDEKRLFALANQKCPNTPPVAGGYSOGAALIAAAVSELG 120  
QY 121 AVKEQKGVAGLFGYTONLQNRGGIPNYPRTKVFNCVNGDAVCTGLTIITPAHLSVTIEA 180  
DB 121 AVKEQKGVAGLFGYTONLQNRGGIPNYPRTKVFNCVNGDAVCTGLTIITPAHLSVTIEA 180  
QY 181 RGEAARFLDRIRA 194  
DB 181 RGEAARFLDRIRA 194  
RESULT 9  
AAB13703  
ID AAB13703 standard; Protein; 194 AA.  
XX

AC AAB13703;  
 XX 17-NOV-2000 (first entry)  
 XX H. insolens mutant cutinase, R51P substitution.  
 XX Site directed mutagenesis; cutinase; mutant; mutein; substitution;  
 KW thermostability; enzyme; lipolytic; fabric finishing; yarn;  
 KW protein co-ordinate.  
 XX Humicola insolens.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 51  
 FT /note= "Wild-type Arg substituted by Pro"  
 XX WO200034450-A1.  
 XX 15-JUN-2000.  
 XX 03-DEC-1999; 99WO-DK00678.  
 XX 04-DEC-1998; 98DK-0001604.  
 PR 09-DEC-1998; 98US-0111591.  
 PR 09-MAR-1999; 99DK-0000330.  
 PR 16-MAR-1999; 99US-0124671.  
 XX (NOVO ) NOVO-NORDISK AS.  
 XX Abo M, Fukuyama S, Svendsen A, Matsui T;  
 XX WPI; 2000-482424/42.  
 XX Thermostable variant of parent fungal cutinase useful for dyeing  
 PT polyester yarn or fabric, comprises substitution of amino acid residues  
 PT at predetermined positions from the N-terminal amino acid -  
 XX Claim 16; Page -; 79pp; English.  
 XX Site-directed mutagenesis was carried out on wild-type Humicola insolens  
 CC cutinase, to produce the present sequence. The introduced substitution  
 CC improves the thermostability of the cutinase enzyme. Cutinases are  
 CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase  
 CC may be used in the enzymatic hydrolysis of cyclic oligomers of  
 CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from  
 CC poly(ethylene terephthalate) fibers. Cutinase variants with improved  
 CC thermostability are useful since they can withstand higher processing  
 CC temperatures.  
 CC Note: the present sequence is not shown in the specification but is  
 CC derived from the H. insolens wild-type cutinase sequence given in SEQ ID  
 CC 2 of patent: US 5,827,719.  
 XX Sequence 194 AA;  
 CC Query Match 99.3%; Score 992; DB 21; Length 194;  
 CC Best Local Similarity 99.5%; Pred. No. 2e-99;  
 CC Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QLGAIENGLESGSNACPDAILIFARGSTEGPNNGITVGPALANGLESHPNINWIOGVGG 60  
 DB 1 QLGAIENGLESGSNACPDAILIFARGSTEGPNNGITVGPALANGLESHPNINWIOGVGG 60  
 QY 61 PYDAALATNPLPGTQSQANDIEGKRLFALANQKCPNTPVVGAGYSQGAALIAAAVSELSG 120  
 DB 61 PYDAALATNPLPGTQSQANDIEGKRLFALANQKCPNTPVVGAGYSQGAALIAAAVSELSG 120  
 QY 121 AVKEQVKGVALFGYTONLQNRGGIPNTPRRTKVFNCVNGDAVCTGTLITPAHLSYITIEA 180  
 DB 121 AVKEQVKGVALFGYTONLQNRGGIPNTPRRTKVFNCVNGDAVCTGTLITPAHLSYITIEA 180  
 QY 181 RGEAARFLRDRIRA 194  
 DB 181 RGEAARFLRDRIRA 194

DB 181 RGEAARFLRDRIRA 194  
 RESULT 10  
 AAB13704  
 ID AAB13704 standard; Protein; 194 AA.  
 XX AAB13704;  
 AC AAB13704;  
 XX 17-NOV-2000 (first entry)  
 XX H. insolens mutant cutinase, E6X/L138I substitution.  
 DE Site directed mutagenesis; cutinase; mutant; mutein; substitution;  
 KW thermostability; enzyme; lipolytic; fabric finishing; yarn;  
 KW protein co-ordinate.  
 XX Humicola insolens.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 6  
 FT /note= "Wild-type Glu substituted by Asn or Gln"  
 FT Misc-difference 138  
 FT /note= "Wild-type Leu substituted by Ile"  
 XX WO200034450-A1.  
 XX 15-JUN-2000.  
 XX 03-DEC-1999; 99WO-DK00678.  
 XX 04-DEC-1998; 98DK-0001604.  
 PR 09-DEC-1998; 98US-0111591.  
 PR 09-MAR-1999; 99DK-0000330.  
 PR 16-MAR-1999; 99US-0124671.  
 XX (NOVO ) NOVO-NORDISK AS.  
 XX Abo M, Fukuyama S, Svendsen A, Matsui T;  
 XX WPI; 2000-482424/42.  
 XX Thermostable variant of parent fungal cutinase useful for dyeing  
 PT polyester yarn or fabric, comprises substitution of amino acid residues  
 PT at predetermined positions from the N-terminal amino acid -  
 XX Claim 16; Page -; 79pp; English.  
 XX Site-directed mutagenesis was carried out on wild-type Humicola insolens  
 CC cutinase, to produce the present sequence. The introduced substitution  
 CC improves the thermostability of the cutinase enzyme. Cutinases are  
 CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase  
 CC may be used in the enzymatic hydrolysis of cyclic oligomers of  
 CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from  
 CC poly(ethylene terephthalate) fibers. Cutinase variants with improved  
 CC thermostability are useful since they can withstand higher processing  
 CC temperatures.  
 CC Note: the present sequence is not shown in the specification but is  
 CC derived from the H. insolens wild-type cutinase sequence given in SEQ ID  
 CC 2 of patent: US 5,827,719.  
 XX Sequence 194 AA;  
 CC Query Match 99.2%; Score 991; DB 21; Length 194;  
 CC Best Local Similarity 99.0%; Pred. No. 2.5e-99;  
 CC Matches 192; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 QLGAIENGLESGSNACPDAILIFARGSTEGPNNGITVGPALANGLESHPNINWIOGVGG 60  
 DB 1 QLGAIENGLESGSNACPDAILIFARGSTEGPNNGITVGPALANGLESHPNINWIOGVGG 60  
 QY 61 PYDAALATNPLPGTQSQANDIEGKRLFALANQKCPNTPVVGAGYSQGAALIAAAVSELSG 120



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Db 61 PYDAALATNPLPGTSQANIDEGKRLFALANQKCPNTPPVAGGYSQGAALIAAASVLSG 120
      |||
QY 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVGDVCTGTLITPAHLSYTTIEA 180
      |||
Db 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVGDVCTGTLITPAHLSYTTIEA 180
      |||
QY 181 RGEAARFLDRIRA 194
      |||
Db 181 RGEAARFLDRIRA 194
      |||

RESULT 11
ABB76845
ID ABB76845 standard; Protein; 194 AA.
XX
AC ABB76845;
XX
DT 25-JUN-2002 (first entry)
XX
DE Mutant Humicola insolens mature cutinase #19.
XX
KW Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
XX
OS Humicola insolens strain DSM 1800.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Wild-type Gln substituted by Cys"
FT FT
FT Misc-difference 2 /note= "Wild-type Leu substituted by Val"
XX
PN W0200192502-A1.
XX
PD 06-DEC-2001.
XX
PF 22-MAY-2001; 2001WO-DK00350.
XX
PR 02-JUN-2000; 2000DK-0000861.
PR 23-OCT-2000; 2000DK-0001577.
PR 24-NOV-2000; 2000DK-0001772.
PR 19-JAN-2001; 2001DK-0000100.
XX
PA (NOVO ) NOVOZYMES AS.
XX
PI Svendsen A, Glad SOS, Fukuyama S, Matsui T;
XX
DR WPI; 2002-216714/27.
XX
PT Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
PT oligomers of poly(ethylene terephthalate), comprises a substitution of
PT amino acid residues corresponding to positions of Humicola insolens
PT cutinase -
XX
PS Claim 8; Page -; 41pp; English.
XX
CC The present invention relates to wild-type mature cutinase from Humicola
CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant
CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic
CC enzymes capable of hydrolyzing the substrate cutin. The mutant cutinases
CC have improved thermostability, and are used for enzymatic hydrolysis
CC of cyclic oligomers of poly(ethylene terephthalate), e.g. in the
CC finishing of yarn or fabric from poly(ethylene terephthalate) fibers.
CC Note: the present sequence in not shown in the specification, but is
CC derived from the wild-type cutinase sequence shown on page 36.
XX
SQ Sequence 194 AA;
XX
Query Match 99.2%; Score 991; DB 23; Length 194;
Best Local Similarity 99.5%; Pred. No. 2.5e-99;
Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 LGAIENGLESANACPDAILIFARGSTEPGNMGITVGPALANGLESIRNIWIQVGGP 61
      |||
Db 2 VGAIEENGLESANACPDAILIFARGSTEPGNMGITVGPALANGLESIRNIWIQVGGP 61
      |||
QY 62 YDAALATNPLPGTSQANIDEGKRLFALANQKCPNTPPVAGGYSQGAALIAAASVLSGA 121
      |||
Db 62 YDAALATNPLPGTSQANIDEGKRLFALANQKCPNTPPVAGGYSQGAALIAAASVLSGA 121
      |||
QY 122 VKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVGDVCTGTLITPAHLSYTTIEAR 181
      |||
Db 122 VKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVGDVCTGTLITPAHLSYTTIEAR 181
      |||
QY 182 GEAARFLDRIRA 194
      |||
Db 182 GEAARFLDRIRA 194
      |||

RESULT 12
AAR95051
ID AAR95051 standard; Protein; 246 AA.
XX
AC AAR95051;
XX
DT 17-DEC-1996 (first entry)
XX
DE H. insolens lipase.
XX
KW lipase; detergent; dishwashing; laundry; short-chain lipid.
XX
OS Humicola insolens.
XX
FH Key Location/Qualifiers
FT Peptide 1..35
FT /label= signal_peptide
FT Protein 36..246
FT /label= mature_protein
XX
PN W09613580-A1.
XX
PD 09-MAY-1996.
XX
PF 26-OCT-1995; 95WO-DK00427.
XX
PR 26-OCT-1994; 94DK-0001240.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Kauppinen S, Kofod LV, Sandal T;
XX
DR WPI; 1996-239493/24.
DR N-PSDB; AAR29401.
XX
PT Isolated DNA encoding lipolytic enzyme - derived from Humicola
PT insolens DSM1800, used partic. as detergent additive for laundry and
PT dishwashing compsns.
XX
PS Disclosure; Page 52; 63pp; English.
XX
CC The present sequence is that of an enzyme with lipolytic activity,
CC derived from Humicola insolens DSM1800. The enzyme has a mol. wt. of
CC about 20-21 kDa, a pI in the range of 709, a pH optimum of about 8 and
CC has specificity towards short-chain lipid substrates. It can be used as
CC a detergent additive, partic. in compsns. for laundry washing or
CC dishwashing.
XX
SQ Sequence 246 AA;
XX
Query Match 99.2%; Score 991; DB 17; Length 246;
Best Local Similarity 99.5%; Pred. No. 3.5e-99;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 QLCGAIENGLESANACPDAILIFARGSTEPGNMGITVGPALANGLESIRNIWIQVGG 60
      |||
```

Db 36 QLGAIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLSHIRNIWIOGVGG 95  
QY 61 PYDAALATNPLPRGTSQANIDEGKRLFALANOKCPNTPVAGGYSGAALIAAAVSELGG 120  
Db 96 PYDAALATNPLPRGTSQANIDEGKRLFALANOKCPNTPVAGGYSGAALIAAAVSELGG 155  
QY 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVGDVAVCTGTLITPAHLSYTTIEA 180  
Db 156 AVKEQVKGVALFGYTONLQNRGGIANYPRTKVFNCVGDVAVCTGTLITPAHLSYTTIEA 215  
QY 181 RGEAARFLDRIRA 194  
Db 216 RGEAARFLDRIRA 229  
RESULT 13  
AAB13705  
ID AAB13705 standard; Protein; 194 AA.  
XX  
AC AAB13705;  
XX  
DT 17-NOV-2000 (first entry)  
XX  
DE H. insolens mutant cutinase, A14P/E47K substitution.  
XX  
KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;  
KW thermostability; enzyme; lipolytic; fabric finishing; yarn;  
KW protein co-ordinate.  
XX  
OS Humicola insolens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 14  
FT /note= "Wild-type Ala substituted by Pro"  
FT  
FT Misc-difference 47  
FT /note= "Wild-type Glu substituted by Lys"  
XX  
PN WO200034450-A1.  
XX  
PD 15-JUN-2000.  
XX  
XX 03-DEC-1999; 99WO-DK00678.  
XX  
XX 04-DEC-1998; 98DK-0001604.  
PR 09-DEC-1998; 98US-0111591.  
PR 09-MAR-1999; 99DK-0000330.  
PR 16-MAR-1999; 99US-0124671.  
XX  
PA (NOVO ) NOVO-NORDISK AS.  
XX  
XX Abo M, Fukuyama S, Svendsen A, Matsui T;  
XX WPI; 2000-482424/42.  
XX  
XX Thermostable variant of parent fungal cutinase useful for dyeing  
PT polyester yarn or fabric, comprises substitution of amino acid residues  
PT at predetermined positions from the N-terminal amino acid  
XX  
XX Claim 16; Page -: 79pp; English.  
XX  
XX Site-directed mutagenesis was carried out on wild-type Humicola insolens  
CC cutinase, to produce the present sequence. The introduced substitution  
CC improves the thermostability of the cutinase enzyme. Cutinases are  
CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase  
CC may be used in the enzymatic hydrolysis of cyclic oligomers of  
CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from  
CC poly(ethylene terephthalate) fibers. Cutinase variants with improved  
CC thermostability are useful since they can withstand higher processing  
CC temperatures.  
CC  
CC Note: the present sequence is not shown in the specification but is  
CC derived from the H. insolens wild-type cutinase sequence given in SEQ ID  
CC 2 of patent: US 5,827,719.

XX Sequence 194 AA;  
SQ  
Query Match 99.1%; Score 990; DB 21; Length 194;  
Best Local Similarity 99.0%; Pred. No. 3.2e-99;  
Matches 192; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QLGAIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLSHIRNIWIOGVGG 60  
Db 1 QLGAIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLSHIRNIWIOGVGG 60  
QY 61 PYDAALATNPLPRGTSQANIDEGKRLFALANOKCPNTPVAGGYSGAALIAAAVSELGG 120  
Db 61 PYDAALATNPLPRGTSQANIDEGKRLFALANOKCPNTPVAGGYSGAALIAAAVSELGG 120  
QY 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVGDVAVCTGTLITPAHLSYTTIEA 180  
Db 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRTKVFNCVGDVAVCTGTLITPAHLSYTTIEA 180  
QY 181 RGEAARFLDRIRA 194  
Db 181 RGEAARFLDRIRA 194  
RESULT 14  
AAB13711  
ID AAB13711 standard; Protein; 194 AA.  
XX  
AC AAB13711;  
XX  
DT 17-NOV-2000 (first entry)  
XX  
DE H. insolens mutant cutinase, E47K/D63N substitution.  
XX  
KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;  
KW thermostability; enzyme; lipolytic; fabric finishing; yarn;  
KW protein co-ordinate.  
XX  
OS Humicola insolens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 47  
FT /note= "Wild-type Glu substituted by Lys"  
FT  
FT Misc-difference 63  
FT /note= "Wild-type Asp substituted by Asn"  
XX  
PN WO200034450-A1.  
XX  
PD 15-JUN-2000.  
XX  
XX 03-DEC-1999; 99WO-DK00678.  
XX  
XX 04-DEC-1998; 98DK-0001604.  
PR 09-DEC-1998; 98US-0111591.  
PR 09-MAR-1999; 99DK-0000330.  
PR 16-MAR-1999; 99US-0124671.  
XX  
PA (NOVO ) NOVO-NORDISK AS.  
XX  
XX Abo M, Fukuyama S, Svendsen A, Matsui T;  
XX WPI; 2000-482424/42.  
XX  
XX Thermostable variant of parent fungal cutinase useful for dyeing  
PT polyester yarn or fabric, comprises substitution of amino acid residues  
PT at predetermined positions from the N-terminal amino acid  
XX  
XX Claim 16; Page -: 79pp; English.  
XX  
XX Site-directed mutagenesis was carried out on wild-type Humicola insolens  
CC cutinase, to produce the present sequence. The introduced substitution  
CC improves the thermostability of the cutinase enzyme. Cutinases are

CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase  
CC may be used in the enzymatic hydrolysis of cyclic oligomers of  
CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from  
CC poly(ethylene terephthalate) fibers. Cutinase variants with improved  
CC thermostability are useful since they can withstand higher processing  
CC temperatures.  
CC Note: the present sequence is not shown in the specification but is  
CC derived from the H. insolens wild-type cutinase sequence given in SEQ ID  
CC 2 of patent: US 5,827,719.

XX Sequence 194 AA;

Query Match 99.1%; Score 990; DB 21; Length 194;  
Best Local Similarity 99.0%; Pred. No. 3.2e-99;  
Matches 192; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVG 60  
DB 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVG 60  
QY 61 PYDAALATNLFPRGTQANIDEKRLFALANOKCPNTPVVAGGYSOGAALIAAAVSELG 120  
DB 61 PYDAALATNLFPRGTQANIDEKRLFALANOKCPNTPVVAGGYSOGAALIAAAVSELG 120  
QY 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRETRKVFNCVGDVCTGLTIITPAHLSYTTIEA 180  
DB 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRETRKVFNCVGDVCTGLTIITPAHLSYTTIEA 180  
QY 181 RGEAARFLDRIR 194  
DB 181 RGEAARFLDRIR 194

RESULT 15  
ABB76829  
ID ABB76829 standard; Protein; 194 AA.  
XX ABB76829;  
AC  
XX  
XX 25-JUN-2002 (first entry)  
DE Mutant Humicola insolens mature cutinase #3.  
XX  
XX Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.  
XX  
XX Humicola insolens strain DSM 1800.  
OS Synthetic.

XX Key Location/Qualifiers  
FT Misc-difference 44  
FT /note= "Wild-type Asn substituted by Asp"  
FT Misc-difference 130  
FT /note= "Wild-type Ala substituted by Val"  
XX  
PN WO200192502-A1.  
XX  
XX 06-DEC-2001.  
XX  
XX 22-MAY-2001; 2001WO-DK00350.  
XX  
XX 02-JUN-2000; 2000DK-0000861.  
PR 23-OCT-2000; 2000DK-0001577.  
PR 24-NOV-2000; 2000DK-0001772.  
PR 19-JAN-2001; 2001DK-0000100.  
XX  
XX (NOVO ) NOVOZYMES AS.  
XX  
XX Svendsen A, Glad SO5, Fukuyama S, Matsui T;  
PI  
XX WPI; 2002-216714/27.  
XX  
XX Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic  
PT oligomers of poly(ethylene terephthalate), comprises a substitution of

PT. amino acid residues corresponding to positions of Humicola insolens  
cutinase -  
XX  
PS Claim 8; Page -; 4lpp; English.  
XX  
CC The present invention relates to wild-type mature cutinase from Humicola  
insolens strain DSM 1800 (AAM48435), which was used to generate mutant  
cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic  
enzymes capable of hydrolysing the substrate cutin. The mutant cutinases  
have improved thermostability, and are used for enzymatic hydrolysis  
of cyclic oligomers of poly(ethylene terephthalate), e.g. in the  
finishing of yarn or fabric from poly(ethylene terephthalate) fibers.  
CC Note: the present sequence is not shown in the specification, but is  
derived from the wild-type cutinase sequence shown on page 36.

XX Sequence 194 AA;

Query Match 99.1%; Score 990; DB 23; Length 194;  
Best Local Similarity 99.0%; Pred. No. 3.2e-99;  
Matches 192; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVG 60  
DB 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVG 60  
QY 61 PYDAALATNLFPRGTQANIDEKRLFALANOKCPNTPVVAGGYSOGAALIAAAVSELG 120  
DB 61 PYDAALATNLFPRGTQANIDEKRLFALANOKCPNTPVVAGGYSOGAALIAAAVSELG 120  
QY 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRETRKVFNCVGDVCTGLTIITPAHLSYTTIEA 180  
DB 121 AVKEQVKGVALFGYTONLQNRGGIPNYPRETRKVFNCVGDVCTGLTIITPAHLSYTTIEA 180  
QY 181 RGEAARFLDRIR 194  
DB 181 RGEAARFLDRIR 194

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Job time : 37 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 2, 2003, 15:06:24 ; Search time 10 Seconds  
(without alignments)  
367.659 Million cell updates/sec

Title: US-09-873-075A-1

Perfect score: 999

Sequence: 1 QLGAIENGLESANACPD.....SYTIEARGEARFLDRIRA 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA.\*

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2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	999	100.0	194	10 US-09-873-075A-1	Sequence 1, Appli
2	268	26.8	255	9 US-10-114-116-1	Sequence 1, Appli
3	268	26.8	255	9 US-10-114-115A-1	Sequence 1, Appli
4	197.5	19.8	217	10 US-09-791-171-10	Sequence 10, Appl
5	187.5	18.8	219	10 US-09-791-171-14	Sequence 14, Appl
6	179	17.9	226	10 US-09-791-171-52	Sequence 52, Appl
7	167.5	16.8	262	10 US-09-791-171-56	Sequence 56, Appl
8	145	14.5	285	9 US-10-051-643-197	Sequence 197, App
9	119	11.9	748	9 US-10-051-643-154	Sequence 154, App
10	116	11.6	167	9 US-10-051-643-112	Sequence 112, App
11	86.5	8.7	200	10 US-09-950-368-18	Sequence 18, Appl
12	83	8.3	1356	9 US-10-077-111-10	Sequence 10, Appl
13	82.5	8.3	309	10 US-09-815-242-11920	Sequence 11920, A
14	76.5	7.7	309	9 US-09-738-626-6668	Sequence 6668, Ap
15	76.5	7.7	1008	12 US-10-017-828-7	Sequence 7, Appli
16	76.5	7.7	1008	12 US-10-017-828-8	Sequence 8, Appli
17	76	7.6	424	10 US-09-815-242-13704	Sequence 13704, A
18	74	7.4	1293	10 US-09-815-242-10079	Sequence 10079, A
19	73	7.3	1454	10 US-09-854-799-22	Sequence 22, Appl

20	73	7.3	1454	10 US-09-854-799-26	Sequence 26, Appl
21	72	7.2	341	9 US-09-738-626-6080	Sequence 6080, Ap
22	72	7.2	424	10 US-09-815-242-10252	Sequence 10252, A
23	72	7.2	778	10 US-09-841-132-193	Sequence 193, App
24	72	7.2	978	12 US-10-007-693-65	Sequence 65, Appl
25	72	7.2	1530	10 US-09-841-132-178	Sequence 178, App
26	71.5	7.2	582	10 US-09-815-242-13898	Sequence 13898, A
27	71	7.1	1531	12 US-10-007-693-98	Sequence 98, Appl
28	70.5	7.1	144	10 US-09-923-299-810	Sequence 810, App
29	70	7.0	617	10 US-09-815-242-13228	Sequence 13228, A
30	70	7.0	1344	9 US-09-738-626-6888	Sequence 6888, Ap
31	70	7.0	1616	9 US-09-712-363-262	Sequence 262, App
32	69.5	7.0	399	9 US-09-738-626-4632	Sequence 4632, Ap
33	69.5	7.0	572	10 US-09-815-242-10049	Sequence 10049, A
34	69	6.9	261	10 US-09-940-037A-29	Sequence 29, Appl
35	69	6.9	334	9 US-09-738-626-3582	Sequence 3582, Ap
36	69	6.9	406	10 US-09-815-242-12004	Sequence 12004, A
37	69	6.9	426	9 US-10-124-800-10	Sequence 10, Appl
38	69	6.9	611	10 US-09-748-107-4	Sequence 4, Appl1
39	69	6.9	694	9 US-09-738-626-3867	Sequence 3867, Ap
40	69	6.9	1454	10 US-09-854-799-32	Sequence 32, Appl
41	69	6.9	2910	9 US-10-124-800-2	Sequence 2, Appl1
42	68	6.8	315	10 US-09-764-853-793	Sequence 793, App
43	68	6.8	1510	9 US-09-738-626-3707	Sequence 3707, Ap
44	67.5	6.8	460	9 US-09-813-453A-39	Sequence 39, Appl
45	67.5	6.8	516	9 US-09-738-626-6665	Sequence 6665, Ap

#### ALIGNMENTS

RESULT 1  
US-09-873-075A-1  
; Sequence 1, Application US/09873075A  
; Patent No. US20020123123A1  
; GENERAL INFORMATION:  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Schroder Glad, Sanne  
; APPLICANT: Fukuyama, Shiro  
; APPLICANT: Matsui, Tomoko  
; TITLE OF INVENTION: Cutinase variants  
; FILE REFERENCE: 10038.200-US  
; CURRENT APPLICATION NUMBER: US/09/873,075A  
; CURRENT FILING DATE: 2001-06-01  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; TYPE: PRT  
; ORGANISM: Humicola insolens  
US-09-873-075A-1

Query Match 100.0%; Score 999; DB 10; Length 194;  
Best Local Similarity 100.0%; Pred. No. 1.8e-93;  
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	QLGAIENGLESANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIOGVG	60
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QY	61	PYDAALATNFLPRGTQSANDIEGKRLFALANOKCPTPVVAGGYSGAALIAAAVSELG	120
Db	61	PYDAALATNFLPRGTQSANDIEGKRLFALANOKCPTPVVAGGYSGAALIAAAVSELG	120
QY	121	AVKEQVGVALLFGYTONLNRGIGIPNYPRRTKVFNCVGDVCTGTLITPAHLSYITIA	180
Db	121	AVKEQVGVALLFGYTONLNRGIGIPNYPRRTKVFNCVGDVCTGTLITPAHLSYITIA	180
QY	181	RGEARFLDRIRA 194	
Db	181	RGEARFLDRIRA 194	



```
; APPLICANT: WELDLINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-14

Query Match 18.8%; Score 187.5; DB 10; Length 219;
Best Local Similarity 31.7%; Pred. No. 1.1e-11;
Matches 66; Conservative 32; Mismatches 75; Indels 35; Gaps 11;

QY 8 GLESGANACPDAILIFARGSTEGNMGITVGPALANGLSHI-RNIWIQVGGPYDAAL 66
Db 25 GAVAPATAACPDAEVFEARGFEPGIG-TVGNFVSALRSKVNKNVAVKYPAD--- 80

QY 67 ATNPLPGTQANIDEKRLFALANQKCPNTPVVGYSOGAA---LIAAVSLSGAVK 123
Db 81 --NQIDVGAN---DMSAHQISMAN-SCPNTRLVPGYSLGAAVTDVVLAVPTQMWGFTN 133

QY 124 -----EQVKGVALFGYTONLQNRGGIPNYP---RERTKVCNVDGAVCTGTLII--- 170
Db 134 PLPPGSDHEHTAVALFG--NGSQWVGPIITFSPAYNDRTIELCHGDGDPVCHPADPNTWEA 191

QY 171 --PAHLSYTIARG---EAAERFLRDRI 193
Db 192 NWPHLAGAYVSSGMVNOADEFVAGKQ 219

RESULT 6
US-09-791-171-52
; Sequence 52, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDLINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-14
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; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-52

Query Match 17.9%; Score 179; DB 10; Length 226;
Best Local Similarity 32.5%; Pred. No. 8.4e-11;
Matches 63; Conservative 24; Mismatches 75; Indels 32; Gaps 11;

QY 17 CPDAILIFARGSTEGNMGITVGPALANGLSHI-RNIWIQVGGPYDAALATNPLPRGT 75
Db 47 CPDAEVVFARGTGEPPGLG-RVGOAFVSSLRQQTINKSIGTYGVNYPANG----DFLAAD 101

QY 76 SQANIDEGKRLFALANQKCPNTPVVGYSOGAA---LIAAA-----VSELSGAVKEQ 125
Db 102 GANDASDHIOQMASA---CRATRLVLGGYSQGAVIDIVTAAPLPGLGFTQPLPPAADH 158

QY 126 VKGVALFGYTONLQNRGG-----IPNYPRETRKVCNVDGAVCT-GTLIIIPAHLSTYI 178
Db 159 IAAIALFG---NPSGRAGGLMSALTPOF-GSKTINLCNNGDPICSDGNR--WRAHLGYVP 212

QY 179 EARGEAAARFLRDRI 192
Db 213 GMTNOAARFVASRI 226

RESULT 7
US-09-791-171-56
; Sequence 56, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDLINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-56

Query Match 16.8%; Score 167.5; DB 10; Length 262;
Best Local Similarity 32.1%; Pred. No. 1.5e-09;
Matches 68; Conservative 22; Mismatches 67; Indels 55; Gaps 13;

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Db 41 ADGCPDAEVTFARGTGPPEGIG-RVGOAFVDSL------QQTGMGICGVYPVNVAASR 91

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Db 150 AAYADNVAAVVFG-----NPSNRAGGSLSLPLFGSKAIDL-CNTPDPIC-----H 196  
QY 174 LSYTIEARG-----EAARFLRDRIRA 194  
Db 197 VGPNGEFGHIDGYIPTTYTQRAASFVVQRLRA 228

## RESULT 8

US-10-051-643-197

; Sequence 197, Application US/10051643

; Publication No. US20020197265A1

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Tan, Paul L. J.

; TITLE OF INVENTION: Methods and Compounds for the Treatment

; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory

; FILE REFERENCE: 11000.1008c2

; CURRENT APPLICATION NUMBER: US/10/051,643

; CURRENT FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: US09/156,181

; PRIOR FILING DATE: 1998-09-17

; PRIOR APPLICATION NUMBER: US 08/996,624

; PRIOR FILING DATE: 1997-12-23

; NUMBER OF SEQ ID NOS: 208

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 197

; LENGTH: 285

; TYPE: PRT

; ORGANISM: Mycobacterium vaccae

US-10-051-643-197

## Query Match

Best Local Similarity 14.5%; Score 145; DB 9; Length 285;

; Publication No. US20020197265A1

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Tan, Paul L. J.

; TITLE OF INVENTION: Methods and Compounds for the Treatment

; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory

; FILE REFERENCE: 11000.1008c2

; CURRENT APPLICATION NUMBER: US/10/051,643

; CURRENT FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: US09/156,181

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 208

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 197

; LENGTH: 285

; TYPE: PRT

; ORGANISM: Mycobacterium vaccae

US-10-051-643-197

## RESULT 9

US-10-051-643-154

; Sequence 154, Application US/10051643

; Publication No. US20020197265A1

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Tan, Paul L. J.

; TITLE OF INVENTION: Methods and Compounds for the Treatment

; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory

; FILE REFERENCE: 11000.1008c2

; CURRENT APPLICATION NUMBER: US/10/051,643

; CURRENT FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: US09/156,181

; PRIOR FILING DATE: 1998-09-17

; PRIOR APPLICATION NUMBER: US 08/996,624  
; PRIOR FILING DATE: 1997-12-23  
; NUMBER OF SEQ ID NOS: 208  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 154  
; LENGTH: 748  
; TYPE: PRT  
; ORGANISM: Mycobacterium vaccae  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (119)...(119)  
US-10-051-643-154

## Query Match

Best Local Similarity 11.9%; Score 119; DB 9; Length 748;

; Publication No. US20020197265A1

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Tan, Paul L. J.

; TITLE OF INVENTION: Methods and Compounds for the Treatment

; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory

; FILE REFERENCE: 11000.1008c2

; CURRENT APPLICATION NUMBER: US/10/051,643

; CURRENT FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: US09/156,181

; PRIOR FILING DATE: 1998-09-17

; PRIOR APPLICATION NUMBER: US 08/996,624

; PRIOR FILING DATE: 1997-12-23

; NUMBER OF SEQ ID NOS: 208

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 112

; LENGTH: 167

; TYPE: PRT

; ORGANISM: Mycobacterium vaccae

; NAME/KEY: UNSURE

; LOCATION: (119)...(119)

US-10-051-643-112

## Query Match

Best Local Similarity 11.6%; Score 116; DB 9; Length 167;

; Publication No. US20020197265A1

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Tan, Paul L. J.

; TITLE OF INVENTION: Methods and Compounds for the Treatment

; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory

; FILE REFERENCE: 11000.1008c2

; CURRENT APPLICATION NUMBER: US/10/051,643

; CURRENT FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: US09/156,181

; PRIOR FILING DATE: 1998-09-17

; PRIOR APPLICATION NUMBER: US 08/996,624

; PRIOR FILING DATE: 1997-12-23

; NUMBER OF SEQ ID NOS: 208

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 112

; LENGTH: 167

; TYPE: PRT

; ORGANISM: Mycobacterium vaccae

; NAME/KEY: UNSURE

; LOCATION: (119)...(119)

US-10-051-643-112

## Query Match

Best Local Similarity 30.1%; Pred. No. 0.00013;

; Publication No. US20020197265A1

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Tan, Paul L. J.

; TITLE OF INVENTION: Methods and Compounds for the Treatment

; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory

; FILE REFERENCE: 11000.1008c2

; CURRENT APPLICATION NUMBER: US/10/051,643

; CURRENT FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: US09/156,181

; PRIOR FILING DATE: 1998-09-17







GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run On: January 2, 2003, 15:04:24 ; Search time 20 Seconds  
(without alignments)  
932.504 Million cell updates/sec

Title: US-09-873-075A-1  
 Perfect score: 999  
 Sequence: 1 QLGAIENGLESGSANACPD.....SYTIEARCEAAARFLDRIRA 194

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 2832224

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

```

```
Database :      PIR_73:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	601.5	60.2	228	1	B20448	cutinase (EC 3.1.1.-
2	584	58.5	224	2	S27451	cutinase (EC 3.1.1.-
3	584	56.5	223	1	S21427	cutinase - fungus
4	558.5	55.9	228	1	S214751	cutinase (EC 3.1.1.-
5	553	55.4	230	1	UVFUS	cutinase (EC 3.1.1.-
6	197.5	19.8	217	2	F70756	probable cutinase
7	187.5	18.8	219	2	A70734	probable cutinase
8	179	17.9	226	2	A70565	probable cutinase
9	167.5	16.8	247	2	H70564	probable cutinase
10	114.5	11.5	187	2	F70796	probable cutinase
11	103	10.3	336	2	F70887	hypothetical prote
12	98	9.8	174	2	G70987	probable cutinase
13	95	9.5	336	2	C85921	conserved hypothet
14	89	8.9	420	2	T35575	hypothetical prote
15	89	8.9	592	1	S13391	endo-1,4-beta-xyla
16	88.5	8.9	317	2	B82637	bifunctional bioti
17	88.5	8.9	6486	2	T31076	tricyclicone synthet
18	88	8.8	3535	2	E83641	probable hemagglut
19	87	8.7	892	2	S76350	hypothetical prote
20	86.5	8.7	123	2	B86656	hypothetical prote
21	86.5	8.7	200	2	A69903	hypothetical prote
22	86	8.6	357	2	A95190	hypothetical prote
23	86	8.6	357	2	B98056	hypothetical prote
24	86	8.6	5627	2	C83339	hypothetical prote
25	84.5	8.5	302	2	S71334	acetyl xylan ester
26	83.5	8.4	338	2	A83846	stage V sporulation
27	83.5	8.4	382	2	A87548	3-carboxy-cis,cis-
28	83	8.3	1293	2	A90707	enterobactin synth
29	83	8.3	1293	2	E85557	enterobactin synth

30	83	8.3	1356	2	T18521
31	83	8.3	8563	2	T30226
32	82.5	8.3	398	2	D83214
33	82.5	8.3	665	2	F97032
34	82.5	8.3	685	2	F30289
35	82	8.2	329	2	B46678
36	82	8.2	619	2	H84116
37	81	8.1	260	2	C83618
38	81	8.1	380	2	B70544
39	80	8.0	466	2	J02263
40	79.5	8.0	459	2	T36334
41	79.5	8.0	749	2	E95889
42	79.5	8.0	2082	2	T37056
43	79	7.9	442	2	A52917
44	79	7.9	462	2	H97691
45	78.5	7.9	243	2	A11049

## ALIGNMENTS

RESULT 1  
S20448 cutinase (BC 3.1.-.-) - rice blast fungus  
C:Species: Magnaporthe grisea (rice blast fungus)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S20448  
R:Swiegard, J.A.; Chumley, F.G.; Valent, B.  
Mol. Gen. Genet. 232, 174-182, 1992  
A:Title: Cloning and analysis of CUT1, a cutinase gene from Magnaporthe grisea.  
A:Reference number: S20448; MUID: 92212279; PMID:1557023  
A:Accession: S20448  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-228 <SWE>  
A:Cross-references: GB:X61500; NID:g2928; PIDN:CAA43717.1; PID:g1045205  
C:Genetics:  
A:Gene: CUT1  
C:Superfamily: cutinase  
C:Keywords: hydrolase

Query Match	60.2%	Score	601.5	DB	1	Length	228		
Best Local Similarity	60.0%	Pred. No.	1.6e-45						
Matches	117	Conservative	27	Mismatches	50	Indels	1	Gaps	1

  

QY	1	QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHRN-IWIOQVG	59
DB	33	QLNSVRNDLISGNAACPVSIIIFARASGEVNGLSAGTIVASLEREFNRNDIWQVG	92
QY	60	GPYDAALATNPLRGTSQANTIDEGKRFLALANQKCPNTPVVVAGGYSQGAALIAAAVSELS	119
DB	93	DPYDAALSPNPLPAGTTQGAIDEAKRMFTLANTKCPNAAVVAGGYSQGTAVMFNAVSEMP	152
QY	120	GAVKEOVKGVALFCYTONLNRGGIPNYPRERTKVCNVGDAVCTGTLITPAHLSTYIE	179
DB	153	AAVDQILGVVFGYITKMLNLRGRIPDPTKEVTEYASDAVCGTGLFLPAHFLYITTE	212
QY	180	ARGEAAARFLDRIRA	194
DB	213	SSIAAPNWLROIIRA	227

RESULT 2  
B27451  
cutinase (EC 3.1.-.-) precursor - anthracnose fungus (Colletotrichum gloeosporioides C;Species: Glomerella cingulata, Colletotrichum gloeosporioides C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 03-Mar-1994 C;Accession: B27451  
R;Ettinger, W.F.; Thukral, S.K.; Kolattukudy, P.E.  
Biochemistry 26, 7883-7892, 1987  
A;Title: Structure of cutinase gene, cDNA, and the derived amino acid sequence A;Reference number: A90524  
A;Accession: B27451



R:Lin, T.S.; Kolattukudy, P.E.  
Eur. J. Biochem. 106, 341-351, 1980  
A:Title: Structural studies on cutinase, a glycoprotein containing novel amino acids and  
A:Reference number: A44665; MUID:80245930; PMID:7398618  
A:Contents: annotation; identification of glucuronylated amino end  
C:Comment: This enzyme catalyzes the hydrolysis of cutin, a polyester that forms the str  
C:Genetics: Southern blot results suggest that the genome contains two copies of the cuti

A:Introns: 64/3  
A:Superfamily: cutinase  
C:Keywords: blocked amino end; glycoprotein; hydrolase  
F:1-31/domain: signal sequence #status predicted <SIG>  
F:32-230/Product: cutinase #status predicted <MAT>  
F:32/Modified site: glucuronylated amino end (Gly) (in mature form) #status experimental  
F:125-187/Disulfide bonds: #status experimental  
F:136,204/Active site: Ser, His #status experimental

Query Match 55.4%; Score 553; DB 1; Length 230;  
Best Local Similarity 55.3%; Pred. No. 3e-41;  
Matches 109; Conservative 32; Mismatches 52; Indels 4; Gaps 3;

QY 1 QLG-ATENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHI--RNTWIOG 57  
Db 30 QLGRTRDDLLINGSACRDIIVIIYARGSTETGNLG-TLGFSTASNLESFAGDKGVWIOG 88  
QY 58 VGGPYDAALATNPLRPTSQANIDEGRKLFALANQKCPNTPVAVGGYSOGAALIAAVSE 117  
Db 89 VGGAYRATLGDNALPRTGSAAREMLGLFQQANTKCPDATLAIAGGYSOGAALAAASIED 148  
QY 118 LSGAVKEOVKVALFGYTNQLNRGGIPNTPRRTKVFNCVNGDAVCTGTIIIPAHLSYT 177  
Db 149 LDSAIRDKIAGTVLFGYTKNLNRGRIPNYPADRTKVFNCVNGDAVCTGTIIIPAHLSYT 208

QY 178 IEARGEAAFLRDRIRA 194  
Db 209 PDARGPAPEFLIEKIRA 225

RESULT 6  
F70756  
probable cutinase precursor with N-terminal signal sequence - Mycobacterium tuberculosis  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: F70756

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: F70756

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-217 <COL>  
A:Cross-references: GB:Z74025; GB:AL123456; NID:93261586; PIDN:CAA98399.1; PID:g1403471  
A:Experimental source: strain H37Rv  
C:Genetics:  
A:Gene: Rv1984c  
C:Superfamily: cutinase

Query Match 19.8%; Score 197.5; DB 2; Length 217;  
Best Local Similarity 30.8%; Pred. No. 4.7e-10;  
Matches 61; Conservative 26; Mismatches 88; Indels 23; Gaps 7;

QY 8 GLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHRNTWIOGVGGPYDAALA 67  
Db 26 GGRAAHADPCSDIAVFAFTHQASGLG-DVGEAFVDSITSQ-----VGGRSIGVYA 76  
QY 68 TNFLP-----RGTSQANIDEGRKLFALANQKCPNTPVAVGGYSOGAALIAAVSELSGAVK 123  
Db 77 VNPASDDYASASNGSDDASAHQRTVASCNPTRIVLGGYSOGATVIDLSTAMPAPVA 136

QY 124 EOYKGVALF-----GYTNQLNRGGIPNYP---RERTKVFNCVNGDAVCTGTIIIPAHLS 175  
Db 137 DHVAALVAFCEPSSGSSFMWGGSLPTIGLYSSKTINLCAPDDPICTGGGNIM-AHVS 195  
QY 176 YTIEA-RGEAARFLRDRIR 192  
Db 196 YVQSGMTSQAATFAANRL 213

RESULT 7  
A70734  
probable cutinase precursor - Mycobacterium tuberculosis (strain H37Rv)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: A70734

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: A70734

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-219 <COL>  
A:Cross-references: GB:Z77163; GB:AL123456; NID:93261610; PIDN:CAB00997.1; PID:g14493  
A:Experimental source: strain H37Rv  
C:Genetics:  
A:Gene: RV2301  
C:Superfamily: cutinase

Query Match 18.8%; Score 187.5; DB 2; Length 219;  
Best Local Similarity 31.7%; Pred. No. 3.6e-09;  
Matches 66; Conservative 32; Mismatches 75; Indels 35; Gaps 11;

QY 8 GLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHI-RNTWIOGVGGPYDAAL 66  
Db 25 GAVAPATAACPDAAEVVFAVGREFPPGIG-TVGNAAFVSALRSKVNKNVGVAVKVPAD--- 80  
QY 67 ATNPLRPTSQANIDEGRKLFALANQKCPNTPVAVGGYSOGAA---LIAAVALSELSGAVK 123  
Db 81 --NQIDVGAN---DMSAHIQSMAN-SCPNTRLVPGYSGLGAATVDVVLAVPTQMMGFTN 133

QY 124 -----EOYKGVALFGYTNQLNRGGIPNYP---RERTKVFNCVNGDAVCTGTIIIT--- 170  
Db 134 PLPPGSDERHTAAVALFG--NGSOWVGPITNFPSPAYNDRTIELCHGDDPVCHPADPNTWEA 191  
QY 171 --PAHLSYTTIARG---EAAARFLRDRIR 193  
Db 192 NWPQHLAGAYVSSGMVNNQAADFVAGKLIQ 219

RESULT 8  
A70565  
probable cutinase precursor - Mycobacterium tuberculosis (strain H37Rv)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: A70565

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: A70565

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-226 <COL>  
A:Cross-references: GB:Z95390; GB:AL123456; NID:93261766; PIDN:CAB08718.1; PID:g21043  
A:Experimental source: strain H37Rv  
C:Genetics:





F:39-133/Disulfide bonds: #status predicted  
F:431/530/Active site: Glu #status predicted

Query Match 8.9%; Score 89; DB 1; Length 592;  
Best Local Similarity 24.9%; Pred. No. 5.1;  
Matches 43; Conservative 19; Mismatches 69; Indels 42; Gaps 8;  
  
QY 15 NACPDAILIFARGSTEPGNNGITVGPALANGLESHIRNIWIOGVGGPY-DAAL----- 66  
Db 378 NNIPVKAHTFVWGAQSPSWLNNLSGPPEVAVEIQ-----WIRDYCARYPDTAMIDVVNEA 432  
QY 67 ATNFLPRGTSQANIDEG--KRLPALANQKCPNTPPVVAGY-----SQGAA 109  
Db 433 VPGHQPAGYAQRAFGNNWIQRVFQLARQYCPNSILILNDYNNIRWQHNEFIALAKAQGN 492  
QY 110 LIAAAVVS--ELSGAVKEQVKGVAFQYTONLONRGIPNYPRERTKVCNVD 160  
Db 493 IDAVGLQAHKGMWTAQAQVTA-----IDNIWQVKGKPIYISE-----YDIGD 535

Search completed: January 2, 2003, 15:06:43  
Job time : 21 secs





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Db 13 QASTTRNELETGSSDACPRTTIFARGSTEGACNMGALVGPFTTANALESAYGASNVWVG 72
QY 59 GGPYDAALATNPLRGTSQANIDEGRFLFALANQKCPNTPVVAGYSOGAALIAAAVSEL 118
DB 73 GGPYTAGLVENALPAGTSQAALREAQRLFNLAASKCPNTPITAGGYSOGAAVMSNAIPGL 132
QY 119 SGAVKEQVKGVLFQYTONLQNRGIPNYPRTKVFQNGDAVCTGTLIITPAHLSTYI 178
DB 133 SAAVDQIKGVVLFQYTKNLQNGRIPNPTSKTIYCTGDLVCGNLTGTLIITPAHLSTY 192
QY 179 EARGAARFLDRRI 192
DB 193 EAAVQAPFLRAQI 206

RESULT 2
CUTL_MAGR
ID CUTL_MAGR STANDARD; PRT; 228 AA.
AC P30272;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74).
GN CUTL.
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
OX NCBI_TaxID=148305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4091-5-8;
RX MEDLINE=92212279; PubMed=1557023;
RA Swelgard J.A., Chumley F., Valent B.;
RT "Cloning and analysis of CUT1, a cutinase gene from Magnaporthe
RT grisea.";
RL Mol. Gen. Genet. 232:174-182(1992).
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection.
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X61500; CAA43717.1; ALT_TERM.
DR HSP; P00590; ICUW.
DR InterPro; IPR000675; Cutinase.
DR Pfam; PF01083; Cutinase; 1.
DR PRINTS; PR00129; CUTINASE.
DR PROSITE; PS00155; CUTINASE_1; 1.
DR PROSITE; PS00931; CUTINASE_2; 1.
KW Hydrolase; Serine esterase; Signal; Glycoprotein.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 228 CUTINASE.
FT DISULFID 49 196 BY SIMILARITY.
FT FT 127 189 BY SIMILARITY.
FT ACT_SITE 138 138 BY SIMILARITY.
FT ACT_SITE 193 193 BY SIMILARITY.
FT ACT_SITE 206 206 BY SIMILARITY.
FT CARBOHYD 190 190 .N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 228 AA; 24276 MW; BB0ACE063B9D4627 CRC64;

Query Match 60.28; Score 601.5; DB 1; Length 228;
Best Local Similarity 60.08; Pred. No. 3.1e-44;
Matches 117; Conservative 27; Mismatches 50; Indels 1; Gaps 1;

```

```

QY 1 QLGAIENGLESANACPDAILIFARGSTEGPNNMGITVGPALANGLESHIRN-IWIOGVG 59
DB 33 QLSNVRLDLSGNAACPSVILIFARASGEVGNMGLSAGTNVASRLERFRNDIWWQGVG 92
QY 60 GPYDAALATNPLRGTSQANIDEGRFLFALANQKCPNTPVVAGYSOGAALIAAAVSEL 119
DB 93 DPYDAALSNPFLPAGTQGAIDEAKRMFTLANTRCPNAAVVAGYSOGTAVMFAVSEMP 152
QY 120 GAVKEQVKGVLFQYTONLQNRGIPNYPRTKVFQNGDAVCTGTLIITPAHLSTYIE 179
DB 153 AAVQDQIKGVVLFQYTKNLQNGRIPDPPTKTEVYCNASDAVCFGLTFLPAHFLYITE 212
QY 180 ARGEAARFLDRRI 194
DB 213 SSIAAPNWLIRIRA 227

RESULT 3
CUTL_COLGL
ID CUTL_COLGL STANDARD; PRT; 224 AA.
AC P11373;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74).
GN CUTA.
OS Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella
OS cingulata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC Glomerella.
OX NCBI_TaxID=5457;
RN [1]
RP SEQUENCE FROM N.A.
RA Ettlinger W.F., Thukral S.K., Kolattukudy P.E.;
RT "Structure of cutinase gene, cDNA, and the derived amino acid
RT sequence from phytopathogenic fungi.";
RL Biochemistry 26:7883-7892(1987).
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection.
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By contact with cutin.
CC -!- PTM: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE
CC BRIDGES RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFIDE
CC CATALYTIC RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME.
CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
CC -----
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CC -----
DR EMBL; M21443; AAA33042.1; -.
DR PTR; B27451; B27451.
DR HSP; P00590; ICUW.
DR InterPro; IPR000675; Cutinase.
DR Pfam; PF01083; Cutinase; 1.
DR PRINTS; PR00129; CUTINASE.
DR PROSITE; PS00155; CUTINASE_1; 1.
DR PROSITE; PS00931; CUTINASE_2; 1.
KW Hydrolase; Serine esterase; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 224 CUTINASE.
FT DISULFID 46 194 BY SIMILARITY.
FT DISULFID 125 187 BY SIMILARITY.
FT ACT_SITE 136 136 BY SIMILARITY.

```

[illegible]

```

RESULT 5
CUTI_COLCA
ID CUTI_COLCA STANDARD; PRT; 228 AA.
AC P10951;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74).
DE CUTA.
GN GN
OS Colletotrichum capsici (Anthracnose fungus).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC mitosporic Phyllachoraceae; Colletotrichum.
OC NCBI_TaxID=5456;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=ATCC 48574;
RA Ettinger W.F., Thukral S.K., Kolattukudy P.E.;
RT "Structure of cutinase gene, cDNA, and the derived amino acid
RL sequence from phytopathogenic fungi.";
RL Biochemistry 26:7883-7892(1987).
CC -1- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection.
CC -1- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- INDUCTION: By contact with cutin.
CC -1- PTM: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE
CC CATALYTIC RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFIDE
CC BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME.
CC -1- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M18033; AAA33043.1; --
CC PIR; A27451; A27451.
CC DR HSSP; P00590; ICW.
CC DR InterPro; IPR000675; Cutinase.
CC DR Pfam; PF01083; Cutinase; 1.
CC DR PRINTS; PR00129; CUTINASE

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DR PROSITE; PS00155; CUTINASE\_1; 1.  
 DR PROSITE; PS00931; CUTINASE\_2; 1.  
 KW Hydrolyase; Serine esterase; Signal.  
 FT SIGNAL 1 16  
 FT CHAIN 17 228  
 FT DISULFID 49 198  
 FT ACT\_SITE 129 191  
 FT ACT\_SITE 140 140  
 FT ACT\_SITE 195 195  
 FT ACT\_SITE 208 208  
 SQ SEQUENCE 228 AA; 23714 MW; 3825D42C23DA139B CRC64;

Query Match 55.9%; Score 558.5; DB 1; Length 228;  
 Best Local Similarity 57.7%; Pred. No. 1.4e-40;  
 Matches 109; Conservative 27; Mismatches 50; Indels 3; Gaps 2;

QY 7 NGLESGSANACPDAILIFARGSTEGPNCMGTVPALANGLESH--IRNIWIOGVGGPYDA 64  
 Db 39 NELESGSSNCPKVIIFARASTEPGNCMGTVPALANGLESH--IRNIWIOGVGGPYDA 98  
 QY 65 ALATNF-LPGTQANIDEKRLFALANQKPNTPVAVGGYSGAALIAAAVSELGAVK 123  
 Db 99 DLASNFIIPEGTSRVINEAKRLFTLANTKCPNSAVVAGGYSGTAVMASSISLSSTIQ 158  
 QY 124 EQVKGVALLGYTONLQNRGIPNPRRTKVFNCVGDVACTGTLITPAHLSYTIARGE 183  
 Db 159 NQIKGVVLSAITKNLQNRGIPNPRRTKVFNCVGDVACTGTLITPAHLSYTIARGE 218  
 QY 184 AARFLRDRI 192  
 Db 219 APFLAARI 227

RESULT 6  
 CUTL\_FUSSC STANDARD; PRT; 230 AA.  
 AC Q99174:  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cutinase precursor (EC 3.1.1.74).  
 GN CUTA.  
 OS Fusarium solani (subsp. cucurbitae) (Nectria ipomoeae).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreales; Nectriaceae; Nectria.  
 OX NCBI\_TaxID=57162;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PGB 153;  
 RX MEDLINE=97254398; PubMed=9100380;  
 RA Crowhurst R.N., Binnie S.J., Bowen J.K., Hawthorne B.T., Plummer K.M.,  
 RA Rees-George J., Rikkerink E.H., Templeton M.D.;  
 RT "Effect of disruption of a cutinase gene (cutA) on virulence and  
 RT tissue specificity of Fusarium solani f. sp. cucurbitae race 2 toward  
 RT Cucurbita maxima and C. moschata".  
 RL Mol. Plant Microbe Interact. 10:355-368(1997).  
 CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that  
 CC forms the structure of plant cuticle. Allows pathogenic fungi to  
 CC penetrate through the cuticular barrier into the host plant during  
 CC the initial stage of the fungal infection.  
 CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.

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 CC -----  
 DR EMBL; U63335; AAB05922.1; "

DR HSSP; P00590; 2CUT.  
 DR InterPro; IPR000675; Cutinase.  
 DR Pfam; PF01083; Cutinase; 1.  
 DR PRINTS; PR00129; CUTINASE.  
 DR PROSITE; PS00155; CUTINASE\_1; 1.  
 DR PROSITE; PS00931; CUTINASE\_2; 1.  
 KW Hydrolyase; Serine esterase; Glycoprotein; Signal.  
 FT SIGNAL 1 16  
 FT CHAIN 17 230  
 FT DISULFID 47 194  
 FT DISULFID 125 187  
 FT ACT\_SITE 136 136  
 FT ACT\_SITE 191 191  
 FT ACT\_SITE 204 204  
 SQ SEQUENCE 230 AA; 23902 MW; 05FB3C33326405AA CRC64;

Query Match 55.9%; Score 558; DB 1; Length 230;  
 Best Local Similarity 55.8%; Pred. No. 1.6e-40;  
 Matches 110; Conservative 32; Mismatches 51; Indels 4; Gaps 3;

QY 1 QLG-ATENGLESGSANACPDAILIFARGSTEGPNCMGTVPALANGLESH--IRNIWIOG 57  
 Db 30 QLGRTTRDDLINGNSASCADVIFVARGSTETGNLG-TLGPSIASNLESAFGTDGWIWG 88  
 QY 58 VGGPYDAALATNPLPGTQANIDEKRLFALANQKPNTPVAVGGYSGAALIAAAVSE 117  
 Db 89 VGGVATRLGDNALPRGTSSAAIREMLGLFQQANKCPDATTIAGGYSGAALAAASIED 148  
 QY 118 LSCAVKEQVKGVALLGYTONLQNRGIPNPRRTKVFNCVGDVACTGTLITPAHLSY 177  
 Db 149 LDSAINDKIAGTVLFGYTKNLQNRGIPNPRRTKVFNCVGDVACTGTLITPAHLSY 208  
 QY 178 IEARGEAAARFLRDRI 194  
 Db 209 PDARGPAPEFLIEKVRA 225

RESULT 7  
 CUTL\_FUSSC STANDARD; PRT; 230 AA.  
 AC P00590:  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cutinase 1 precursor (EC 3.1.1.74).  
 GN CUT1 OR CUTA.  
 OS Fusarium solani (subsp. pisi) (Nectria haematococca).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreales; Nectriaceae; Nectria.  
 OX NCBI\_TaxID=70791;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN-T-8;  
 RA Soliday C.L., Flurkey W.H., Okita T.W., Kolattukudy P.E.;  
 RT "Cloning and structure determination of cDNA for cutinase, an enzyme  
 RT involved in fungal penetration of plants".  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3939-3943(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8917761; PubMed=2703464;  
 RA Soliday C.L., Dickman M.B., Kolattukudy P.E.;  
 RT "Structure of the cutinase gene and detection of promoter activity in  
 RT the 5'-flanking region by fungal transformation".  
 RL J. Bacteriol. 171:1942-1951(1989).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RX MEDLINE=92220194; PubMed=3560844;  
 RA Martinez C., de Geus P., Lauwereys M., Matthysens G., Cambillau C.;  
 RT "Fusarium solani cutinase is a lipolytic enzyme with a catalytic  
 RT serine accessible to solvent".  
 RL Nature 356:615-618(1992).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

*Handwritten notes:*  
 F-  
 cutin

RX MEDLINE-94114517; PubMed-8286366;  
RA Martinez C., Nicollas A., van Tilbeurgh H., Egloff M.-P., Cudrey C.,  
RA Verger R., Cambillau C.;  
RT "Cutinase, a lipolytic enzyme with a preformed oxyanion hole.";  
RL Biochemistry 33:83-89(1994).  
RN [5]  
RN X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS).  
RX MEDLINE-97318923; PubMed-9175860;  
RA Longhi S., Czjzek M., Lamzin V., Nicollas A., Cambillau C.;  
RT "Atomic resolution (1.0 A) crystal structure of Fusarium solani  
RT cutinase: stereochemical analysis.";  
RL J. Mol. Biol. 268:779-799(1997).  
RN [6]  
RN X-RAY CRYSTALLOGRAPHY (1.15 ANGSTROMS) OF 33-230.  
RA Nicollas A., Martinez C., Cambillau C.;  
RL Submitted (MAR-1997) to the PDB data bank.  
RN [7]  
RN STRUCTURE BY NMR.  
RX MEDLINE-98046750; PubMed-9385640;  
RA Prompers J.J., Groenewegen A., van Schaik R.C., Pepermans H.A.M.,  
RA Hilbers C.W.;  
RT "1H, 13C, and 15N resonance assignments of Fusarium solani pisi  
RT cutinase and preliminary features of the structure in solution.";  
RL Protein Sci. 6:2375-2384(1997).  
CC -1- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that  
CC forms the structure of plant cuticle. Allows pathogenic fungi to  
CC penetrate through the cuticular barrier into the host plant during  
CC the initial stage of the fungal infection.  
CC -1- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- INDUCTION: By contact with cutin.  
CC -1- PTM: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE  
CC CATALYTIC RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFIDE  
CC BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME.  
CC -1- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.  
CC -----  
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CC -----  
DR EMBL; K02640; AAA33334.1; -;  
DR EMBL; M29759; AAA33335.1; -;  
DR PIR; A00731; UVFUS.  
DR PIR; A32836; A32836.  
DR PDB; 1CUS; 31-JUL-94.  
DR PDB; 2CUT; 31-AUG-94.  
DR PDB; 1CUA; 11-JUL-96.  
DR PDB; 1CUB; 11-JUL-96.  
DR PDB; 1CUC; 11-JUL-96.  
DR PDB; 1CUD; 11-JUL-96.  
DR PDB; 1CUE; 11-JUL-96.  
DR PDB; 1CUF; 11-JUL-96.  
DR PDB; 1CUG; 11-JUL-96.  
DR PDB; 1CUH; 11-JUL-96.  
DR PDB; 1CUI; 11-JUL-96.  
DR PDB; 1CUJ; 11-JUL-96.  
DR PDB; 1CUK; 11-JUL-96.  
DR PDB; 1CUV; 11-JUL-96.  
DR PDB; 1CUW; 11-JUL-96.  
DR PDB; 1CUX; 11-JUL-96.  
DR PDB; 1CUI; 11-JUL-96.  
DR PDB; 1CUZ; 11-JUL-96.  
DR PDB; 1FFA; 08-MAR-96.  
DR PDB; 1FFB; 08-MAR-96.  
DR PDB; 1FFC; 08-MAR-96.  
DR PDB; 1FFD; 08-MAR-96.  
DR PDB; 1FFE; 08-MAR-96.  
DR PDB; 1CFX; 20-AUG-97.  
DR PDB; 10XM; 15-MAY-97.

DR PDB; 1XZA; 14-OCT-96.  
DR PDB; 1XZB; 14-OCT-96.  
DR PDB; 1XZC; 14-OCT-96.  
DR PDB; 1XZD; 14-OCT-96.  
DR PDB; 1XZE; 14-OCT-96.  
DR PDB; 1XZF; 14-OCT-96.  
DR PDB; 1XZG; 14-OCT-96.  
DR PDB; 1XZH; 14-OCT-96.  
DR PDB; 1XZI; 14-OCT-96.  
DR PDB; 1XZJ; 14-OCT-96.  
DR PDB; 1XZK; 30-NOV-96.  
DR PDB; 1XZL; 30-NOV-96.  
DR PDB; 1XZM; 30-NOV-96.  
DR PDB; 1AGY; 01-APR-98.  
DR GlycoSuiteDB; P00590;  
DR InterPro; IPR000675; Cutinase.  
DR Pfam; PF01083; Cutinase; 1.  
DR PRINTS; PR00129; CUTINASE.  
DR PROSITE; PS00155; CUTINASE\_1; 1.  
DR PROSITE; PS00931; CUTINASE\_2; 1.  
KW Hydrolase; Serine esterase; Glycoprotein; Signal; 3D-structure.  
FT SIGNAL 1 16  
FT CHAIN 17 230 CUTINASE 1.  
FT BINDING 32 32 GLUCURONIC ACID.  
FT DISULFID 47 194  
FT DISULFID 125 187  
FT ACT\_SITE 136 136  
FT ACT\_SITE 191 191  
FT ACT\_SITE 204 204  
FT CONFLICT 48 48 R -> A (IN REF. 2).  
FT CONFLICT 94 94 R -> A (IN REF. 2).  
SQ SEQUENCE 230 AA; 23982 MW; 7253ACAA657ADIAB CRC64;  
  
Query Match 55.4%; Score 553; DB 1; Length 230;  
Best Local Similarity 55.3%; Pred. No. 4; le-40;  
Matches 109; Conservative 32; Mismatches 52; Indels 4; Gaps 3;  
  
QY 1 QLG-ATLESGSANACPDALIFARGSTEGPNCNMGTTPGALANGLESHI--RNIIWIOG 57  
DB 30 QLGRTRDDLLINGSACRDVFIYARGSTETGNLG-TLGPSIASNLESFAGDGVWIOG 88  
QY 58 VGGPDAALATNPLPRGTQANIDEKRLFLANQKCPNTPVVAGYSQGAALIAAAVSE 117  
DB 89 VGCAYRATLGDNALPRGTSSAIREMLGLFQQANTKCPDATLIAGGYSQGAALAAASIED 148  
QY 118 LSGAVKEQVKGVALFGYTONLQNRGIPNYPRTKTVFCNVGAVCTGTLLIIPAHLSYT 177  
DB 149 LDSAIRDKIAGTVLFGYTKNLQNRGIPNYPADRTKVCNTGDLVCTGSLIVAAPHLAYG 208  
QY 178 IEARGEAAAREFLDRIRA 194  
DB 209 PDARGPAPEFLIEKVRA 225  
  
RESULT 8  
CUT2\_FUSO STANDARD; PRT; 231 AA.  
ID CUT2\_FUSO  
AC Q96UT0;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cutinase 2 precursor (EC 3.1.1.74).  
GN CUT2  
OS Fusarium solani (subsp. pisi) (Nectria haematococca).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreales; Nectriaceae; Nectria.  
OX NCBI\_TaxID=70791;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=T-8;  
RA Li D., Sirakova T., Rogers L., Ettlinger W.F., Kolattukudy P.E.;  
RT "Regulation of constitutively expressed and induced cutinase genes by  
RT different zinc finger transcription factors in Fusarium solani f. pisi

```

RT (Haematocytaria haematococca).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection (By similarity).
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
CC -----
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CC -----
DR EMBL; AF417004; AAL18696.1; -.
DR InterPro; IPR000675; Cutinase.
DR Pfam; PF01083; Cutinase; 1.
DR PROSITE; PS00155; CUTINASE_1; 1.
DR PROSITE; PS00931; CUTINASE_2; 1.
DR KW Hydrolyase; Serine esterase; Signal.
DR FT SIGNAL 1 16 POTENTIAL.
DR FT CHAIN 17 231 CUTINASE 2.
DR FT DISULFID 48 195 BY SIMILARITY.
DR FT DISULFID 126 188 BY SIMILARITY.
DR FT ACT_SITE 137 137 BY SIMILARITY.
DR FT ACT_SITE 192 192 BY SIMILARITY.
DR FT ACT_SITE 205 205 BY SIMILARITY.
DR SQ SEQUENCE 231 AA; 23332 MW; 8047714A249C756 CRC64;

Query Match 55.1%; Score 550.5; DB 1; Length 231;
Best Local Similarity 55.7%; Pred. No. 6.8e-40;
Matches 108; Conservative 30; Mismatches 53; Indels 3; Gaps 2;

Qy 3 GAIENGLESGSANACPDAILIFARGSTPEPGNMGTVPALANGLESHT--RNIIQGVGG 60
Db 34 GTTRDLTNGNSACADVIFYARGSTETGNLG-TLGPSTASKLESFAFGDGVWIOGVGG 92

Qy 61 PYDAALATNFPRGTSQANIDEGKRLFALANQKCPNTPVAGGYSQGAALTAASVSELG 120
Db 93 AYRATLGDNSLPRTSSAAIREMLGLFQQANTKCPDALTIAAGGYSQGAALGAASVEDLDS 152

Qy 121 AVKEQVGVGVALFGYTONLQNGGIPNPRRTKVCNVGDVAVCTGLTIITPAHLSYITEA 180
Db 153 AIRDKIAGTVLFQYTKNLQNHGRIPNFPADRTKVCNTGDLVCTGSLIIAAPHLYGPD 212

Qy 181 RGEAARFLRDRI 194
Db 213 RGAPEFLIEKVA 226

RESULT 9
CUT3_FUSSO
ID CUT3_FUSSO STANDARD; PRT; 231 AA.
AC Q96US9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase 3 precursor (EC 3.1.1.74).
GN CUT3.
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T-8;
RA Li D., Sirakova T., Rogers L., Ettinger W.F., Kolattukudy P.E.;
RT "Regulation of constitutively expressed and induced cutinase genes by
RT different zinc finger transcription factors in Fusarium solani f. pisi

```

```

RT (Haematocytaria haematococca).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection (By similarity).
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
CC -----
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CC -----
DR EMBL; AF417005; AAL18697.1; -.
DR InterPro; IPR000675; Cutinase.
DR Pfam; PF01083; Cutinase; 1.
DR PROSITE; PS00155; CUTINASE_1; 1.
DR PROSITE; PS00931; CUTINASE_2; 1.
DR KW Hydrolyase; Serine esterase; Signal.
DR FT SIGNAL 1 16 POTENTIAL.
DR FT CHAIN 17 231 CUTINASE 3.
DR FT DISULFID 48 195 BY SIMILARITY.
DR FT DISULFID 126 188 BY SIMILARITY.
DR FT ACT_SITE 137 137 BY SIMILARITY.
DR FT ACT_SITE 192 192 BY SIMILARITY.
DR FT ACT_SITE 205 205 BY SIMILARITY.
DR SQ SEQUENCE 231 AA; 24016 MW; DB39E3EBECDE202 CRC64;

Query Match 54.9%; Score 548.5; DB 1; Length 231;
Best Local Similarity 55.2%; Pred. No. 1e-39;
Matches 107; Conservative 30; Mismatches 54; Indels 3; Gaps 2;

Qy 3 GAIENGLESGSANACPDAILIFARGSTPEPGNMGTVPALANGLESHT--RNIIQGVGG 60
Db 34 GTTRDLTNGNSACADVIFYARGSTETGNLG-TLGPSTASKLESFAFGDGVWIOGVGG 92

Qy 61 PYDAALATNFPRGTSQANIDEGKRLFALANQKCPNTPVAGGYSQGAALTAASVSELG 120
Db 93 AYRATLGDNSLPRTSSAAIREMLGLFQQANTKCPDALTIAAGGYSQGAALGAASVEDLDS 152

Qy 121 AVKEQVGVGVALFGYTONLQNGGIPNPRRTKVCNVGDVAVCTGLTIITPAHLSYITEA 180
Db 153 AIRDKIAGTVLFQYTKNLQNHGRIPNFPADRTKVCNTGDLVCTGSLIIAAPHLYGPD 212

Qy 181 RGEAARFLRDRI 194
Db 213 RGAPEFLIEKVA 226

RESULT 10
CUT1_ASPOR
ID CUT1_ASPOR STANDARD; PRT; 213 AA.
AC P52956;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74) (L1).
GN CUT1.
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 4202;
RX MEDLINE=95220642; PubMed=7705606;
RA Onishi K., Tolda J., Nakazawa H., Sekiguchi J.;
RT "Genome structure and nucleotide sequence of a lipolytic enzyme gene

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Query Match 18.8%; Score 187.5; DB 1; Length 219;



TIGR; MT3557;	-
DR Tuberculin; RV3451;	-
DR InterPro; IPR00675; Cutinase.	
DR Pfam; PF01083; Cutinase; 1.	
DR PROSITE; PS00155; CUTINASE_1; 1.	
DR PROSITE; PS00931; CUTINASE_2; FALSE NEG.	
KW Hypothetical protein; Hydrolase; Serine esterase; Signal;	
KW Complete proteome.	
FT SIGNAL	1
FT CHAIN	26
FT DISULFID	27 247
FT DISULFID	29 180
FT ACT_SITE	99 173
FT ACT_SITE	110 110
FT ACT_SITE	177 177
FT ACT_SITE	191 191
FT CONFLICT	22 22
FT CONFLICT	194 194
FT SEQUENCE	247 AA; 24884 MW; 07B04671A066D5FF CRC64;
Query Match	16.8%; Score 167.5; DB 1; Length 247;
Best Local Similarity	32.1%; Pred. No. 2.4e-07;
Matches 68; Conservative 22; Mismatches 67; Indels 55; Gaps	
QY 14 ANACPDAILIFARGSTPEGNMGITVGPALANGLESHIRNIWIQVG---	GPYDAALATNF 70
DB 26 ADGCPDAEYTFARGTGEPPGGI-RVQAQFVDSL-	-----OQTGMEICVPVVAASR 76
QY 71 LP-RGTSAINDIEGRKLFALANQCPNTPVVAGYSQGAAL--IAAAV-----SELS 11	
DB 77 LQLHGGDGAN-DAISHIKSMAS-SCPNTKLVLGGYSQGATVIDIVAGVPLGSISFGSPLP 13	
QY 120 GAVKEQGVKVALFYTONLQRGG-----IPNPRTPTKVFCNVGDVACTGLTIITPAH 17	
DB 135 AAYADNWAAVAFVG---NPSNRAGSLSSLSPLFGSKAIDL-CNPTDPIC-----H 18	
QY 174 LSYTIEARQ-----EAARFLRDRIIRA 194	
DB 182 VGPNGFEHGHDGYIPTTTTQAASFVQRLRA 213	
RESULT 15	
ID XYNB_PSEFL	
ID XYNB_PSEFL STANDARD; PRT; 592 AA.	
AC P23030;	
DT 01-NOV-1991 (Rel. 20, Created)	
DT 01-NOV-1991 (Rel. 20, Last sequence update)	
DT 15-JUN-2002 (Rel. 41, Last annotation update)	
DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)	
DE (1,4-beta-D-xylan xylanohydrolase B).	
GN XYNB.	
OS Pseudomonas fluorescens.	
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	
OC Pseudomonas.	
OX NCBI_TaxId=294;	
[1]	
RN SEQUENCE FROM N.A., AND SEQUENCE OF 39-56.	
RC STRAIN=Sp. Cellulosa;	
RX MEDLINE=91097447; PubMed=2125205;	
RA Kallett L.E., Poole D.M., Ferreira L.M.A., Durrant A.J.,	
RA Hazlewood G.P., Gilbert H.J.;	
RT "Xylanase B and an arabinofuranosidase from Pseudomonas fluorescens	
RT subsp. cellulosa contain identical cellulose-binding domains and are	
RT encoded by adjacent genes."	
RL Biochem. J. 272:369-376(1990).	
CC -!- FUNCTION: XYLANASE B CONTRIBUTES TO HYDROLYSE HEMICELLULOSE, THE	
CC MAJOR COMPONENT OF PLANT CELL-WALLS.	
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic	
CC linkages in xyans.	
CC -!- PATHWAY: Hemicellulose degradation.	
CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILY F (FAMILY 10 OF GLYCOSYL	
CC HYDROLASES).	
CC -!- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN	
CC (CBD).	

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DR EMBL; X54523; CAA38389.1; -.  
DR PIR; S13391; S13391.  
DR HSSP; P07986; LEXG.  
DR InterPro; IPR001919; Bac\_cellose-band.  
DR InterPro; IPR001000; Glyco\_hydro\_10.  
DR Pfam; PF00331; Glyco\_hydro\_10; 1.  
DR Pfam; PF00553; CBM\_2; 1.  
DR PRINTS; PR00134; GLHYDRLASE10.  
DR PROSITE; PS00591; GLYCOSYL\_HYDROL\_F10; 1.  
DR PROSITE; PS00561; CBD\_BACTERIAL; 1.  
KW Cellulose degradation; Xylan degradation; Hydrolase; Glycosidase;  
KW Signal.  
FT SIGNAL 1 38  
FT CHAIN 39 592  
FT DOMAIN 39 134 ENDO-1,4-BETA-XYLANASE B.  
FT DOMAIN 135 160 CELLULOSE-BINDING (BY SIMILARITY).  
FT DOMAIN 300 320 SER-RICH (LINKER).  
FT ACT\_SITE 431 431 SER-RICH (LINKER).  
FT ACT\_SITE 431 431 PROTON-DONOR (BY SIMILARITY).  
FT ACT\_SITE 530 530 NUCLEOPHILE (BY SIMILARITY).  
FT DISULFID 39 133 BY SIMILARITY.  
SQ SEQUENCE 592 AA; 63410 MW; E081F6308EA2B93A CRC64;

Query Match 8.9%; Score 89; DB 1; Length 592;  
Best Local Similarity 24.9%; Pred No. 2.8;  
Matches 43; Conservative 19; Mismatches 69; Indels 42; Gaps 8;

QY 15 NACPDAILIFARGSTPGNMGITVGPALANGLESHIRNIQGVGGPY-DAAL----- 66  
Db 378 NNIPVKAHTFVWGAQSPSWLNLGSPGVEVAVETEQ-----WIRDYCARYPDTAMIDVVNEA 432  
QY 67 ATNFLPRGTSQANIDEG--KRLFALANQKCPNTPVVGYY-----SQGAA 109  
Db 433 VPGHOPAGYAQAFAGNNWTFQRFQALQYCPNLSILINDYNNIRWQHNEFIALAKAQGY 492  
QY 110 LIAAAVS--ELSGAVKEQVKGVALFGYTONLQNRGIGPNYPRRTKVFNCVGD 160  
Db 493 IDAVGLQAHELKGMTAAQVKTA-----IDNIWNVQVKPIYISE-----YDIGD 535

Search completed: January 2, 2003, 15:05:39  
Job time : 13 secs





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QY 180 ARGEAARFLRDRIRA 194
   ||||| | | | |
Db 190 A-VEAATFAARAKA 203

RESULT 5
Q8X1P1 PRELIMINARY; PRT; 236 AA.
AC Q8X1P1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cutinase.
GN CUT1.
OS Blumeria graminis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
OC Erysiphales; Erysiphaceae; Blumeria.
OX NCBI_TaxID=34373;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Z., Perfect E., Gurr S.J.;
RT "Cutinase gene isolation and functional analysis from Blumeria
   graminis during the barley/powdery mildew interactions.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF326784; AAL67672.1; -.
DR InterPro: IPR000675; Cutinase.
DR Pfam: PF01083; Cutinase; 1.
DR PROSITE: PS00155; CUTINASE_1; UNKNOWN_1.
SQ SEQUENCE 236 AA; 24604 MW; 6528C4F26A4AFCEC CRC64;

Query Match 20.4%; Score 203.5; DB 3; Length 236;
Best Local Similarity 33.8%; Pred. No. 3.7e-09;
Matches 66; Conservative 30; Mismatches 76; Indels 23; Gaps 10;

QY 7 NGLSASANACPAAILIFARGSTEPGNM--GITVGPALANGLESHI--RNIIQGVGGPY 62
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 56 NATENGLTGSCKPILILIFAKGTGNGVGDSSPGPAWFSELRNATGEDKIAVQGV--QY 113
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 63 DAALATNLFPRGTSQANIDEGKRLFALANQ--KCPNTPVAGVSGGAALIAANVSELS 119
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 114 EADV-FGYLVGGDPES-----QNYLTITNOAVTQCPNSKIVIGVSGOAGITINAAQLYS 168
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 120 GAVKEQKGVALFG--YTQNLQNRGTPNPRERTKVFKNVGDVACTGTLLIITPAHLSYT 177
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 169 PLVTSRIAAVLVGDPYDK-----PVGQVSPSSVLICHGDIICTGSGGDP--HLTYS 222
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 178 IEARGEARFLRDR 192
   ||||| | | | | |
Db 223 KNATC-AAKEFLDR 236

RESULT 6
Q06319 PRELIMINARY; PRT; 231 AA.
AC Q06319;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 23.1 kDa protein (serine esterase, cutinase family).
GN RV3452 OR WP3559 OR MYCY13E12.05.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaiia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogg A., McLean J., Moule S., Murphy L.,

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RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
   complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
   laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z95390; CAB08718.1; ALT_INIT.
DR EMBL: AB007160; AAK47898.1; -.
DR HSSP: P00590; 1CUZ.
DR TIGR: MT3559; -.
DR TubercuList: RV3452;
DR InterPro: IPR000675; Cutinase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF01083; Cutinase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 231 AA; 23686 MW; 45943C6B23FEB480 CRC64;

Query Match 17.9%; Score 179; DB 16; Length 231;
Best Local Similarity 32.5%; Pred. No. 3.8e-07;
Matches 63; Conservative 24; Mismatches 75; Indels 32; Gaps 11;

QY 17 CPDAILIFARGSTEPGNMGTITVGPALANGLESHI--RNIIQGVGGPYDAALATNLFPRGT 75
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 52 CPDAEVVFARGTGPGLG-RVGOAFVSSLRQQTNKISGTGVNYPANG----DFLAAAD 106
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 76 SQANIDEGKRLFALANQKCPNTPVAGVSGGA--LIAAA-----VSELSGAVKEQ 125
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 107 GANDASDHIOQMASA---CRATRLVLGGVSGGAVIDVTAAPLGLGFTQPLPPAADH 163
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 126 VKGVALFGYTONLQNRGG-----IPNPRERTKVFKNVGDVACT--GTLLIITPAHLSYTI 178
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 164 IAAATALFG--NPSGRAGGLMSALTPOF-GSKTINLCNNGDPIGSDGNR--WRAHLGYVP 217
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 179 EARGEARFLRDR 192
   ||||| | | | | |
Db 218 GMTNQAAARFVASRI 231

RESULT 7
Q9KK87 PRELIMINARY; PRT; 220 AA.
AC Q9KK87;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Serine esterase cutinase.
OS Mycobacterium avium.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1764;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=969A45; TISSUE=BLOOD;
RA Carroll J.D., Wallace R.C., Keane J., Arbeit R.D.;
RT "Identification of Mycobacterium avium DNA Sequences that Encode
   Exported Proteins by Using phoA Gene Fusions.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF139058; AAF74988.1; -.
DR InterPro: IPR000675; Cutinase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF01083; Cutinase; 1.
DR PROSITE: PS00155; CUTINASE_1; 1.

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DR PROSITE, PS00931; CUTINASE_2; UNKNOWN_1.
SQ SEQUENCE 220 AA; 22394 MW; CBF4F9F47FF65D9C CRC64;

Query Match 16.1%; Score 160.5; DB 2; Length 220;
Best Local Similarity 28.1%; Pred. No. 1.2e-05;
Matches 54; Conservative 35; Mismatches 82; Indels 21; Gaps 8;

QY 13 SANACPDAILIFARGSTEGPNNIGITVPALANGLSHI--RNIIQGVGGPYDAALATNF 70
DB 31 AADPGSDVSVFARGTHOEPGLG-NIGQAFVDSLTSQLGSRVDVYVAVNP-----AND 83
QY 71 LPRGTSQANIDGKRLFLALANOKCPTPVVAGYSQGAALIAAAYSELGAYKEQVKGVA 130
DB 84 DYHNSANAGADASAHVQDTVAACPNRSRLVGLGYSQGSTVIDLATNAMPSPVADHVAAYA 143
QY 131 LF-----GYTONLQNRGNIPNYP---RERTKFCNVGDAVCTGLIITPAHLSYTIEA-- 180
DB 144 LFGEPSSGFSTLMWGQPLPTINPLYGGKTIISLCAPDDPICSGGNGIM-AHVSY-IDAGM 201
QY 181 RGEARFLDRDI 192
DB 202 TAAQATFAANHL 213

RESULT 8
Q9XB09 PRELIMINARY; PRT; 143 AA.
AC Q9XB09;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE RVD2-RV1758 (fragment).
GS Mycobacterium bovis BCG.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=33892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCG-PASTEUR; PubMed=10320585;
RX MEDLINE=99255698; PubMed=10320585;
RA Gordon S.V., Brosch R., Billault A., Garnier T., Eiglmeyer K.,
RA Cole S.T.;
RT "Identification of variable regions in the genomes of tubercle bacilli
using bacterial artificial chromosome arrays."
RL Mol. Microbiol. 32:643-655(1999).
DR EMBL; Y18606; CAB44660.1;
DR HSSP; P00590; 1XZJ.
DR InterPro; IPR000675; Cutinase.
DR Pfam; PF01083; Cutinase; 1.
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 14434 MW; 6CBA62B8174755E7 CRC64;

Query Match 13.2%; Score 132; DB 2; Length 143;
Best Local Similarity 36.6%; Pred. No. 0.0016;
Matches 41; Conservative 19; Mismatches 36; Indels 16; Gaps 7;

QY 13 SANACPDAILIFARGSTEGPNNIGITVPALANGLSHI--RNIIQGVGGPYDAALATNF 70
DB 25 SDGACPDVEVVFARGTGPPGVG-GIGEDFDALRSKIGKSMGVYGVDP-----ATTD 78
QY 71 LPRGTSQANI-DEGKRLFLALANOKCPTPVVAGYSQGAALI-----AAAVSE 117
DB 79 FP--TAMAGIVDAGTHVQTA-ANCPQSKLVGLGFSQGAAYGVFTAAAIPT 127

RESULT 9
O69691 PRELIMINARY; PRT; 207 AA.
AC O69691;
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
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DE Putative cutinase precursor (Serine esterase, cutinase family).
GS RV3724 OR MT3827 OR MTV025.072.
ON Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022121; CAA18046.1; ALT_INIT.
DR EMBL; AE007179; AAK48196.1;
DR TIGR; MT3827;
DR TubercuList; RV3724;
DR InterPro; IPR000675; Cutinase.
DR Pfam; PF01083; Cutinase; 1.
KW Complete proteome.
SQ SEQUENCE 207 AA; 21225 MW; 967510FD7C49D7D5 CRC64;

Query Match 11.5%; Score 114.5; DB 16; Length 207;
Best Local Similarity 26.4%; Pred. No. 0.071;
Matches 43; Conservative 22; Mismatches 75; Indels 23; Gaps 6;

QY 51 RNIIQGVGGPYDAALATNLPRTGSQANIDGKRLFLALANOKCPTPVVAGYSQGAAL 110
DB 47 KSLGVYAVNYPASNDPFSDDPKTVIDGIRDAGSHIQSMA-MSCPQTRQVLGGYSQGA 105
QY 111 -----TAAAVSELGAVKEQVKGVALFG--YTQNLRNGGIP----NYPRE 150
DB 106 AGYVTSVAVVPVPAVPOAVPAPMAPEVANHVAATVLFGAQFLGOYGAPPIAIGPLQ 165
QY 151 RTKVPNCVGDVCTGLIITPAHLSYTTIAR-GEAARFLDRDI 192
DB 166 KTLQLCADGDSIC-GDGNSPVAGHLYAVNGVMVGOGANFAASRL 207

RESULT 10
O59893 PRELIMINARY; PRT; 234 AA.
AC O59893;
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Acetyl xylan esterase II (EC 3.1.1.6).
GN AXE-2.
OS Penicillium purpogenum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiata; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=28575;
RN [1]
RP SEQUENCE FROM N.A.
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[illegible]

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DR TIGR; MT1805; --
DR Tuberculin; Rv1758; --
DR InterPro; IPR000675; Cutinase.
DR Pfam; PF01083; Cutinase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 174 AA; 17868 MW; 36684DEB29AE73C8 CRC64;

Query Match          9.8%; Score 98; DB 16; Length 174;
Best Local Similarity 29.9%; Pred. No. 1.3;
Matches 52; Conservative 22; Mismatches 64; Indels 36; Gaps 12;

Qy 44 NGLSHI--RNIIWIOGVGPGYDAALATNPLPGTSGQANI--DEGKRLFALANQKCPNTPV 100
Db 11 DALRSKIGEKSGVGVGVDP-----ATTDFP--TAMAGIYDAGTHVEQTA--ANCPQSKLV 62

Qy 101 AGGYSGQAALI-----AAAVSE-----LSGAVKEOVKGVALFGY--TONLQNRGGIP 145
Db 63 LGGFSGQRAVMGVFTRAAIPDGPALDAPRPMPPEVADHVAATLFGMFSVAFMHISIGAPP 122

Qy 146 ----NYPRTKVFNCVGDVCT--GTIIITPAHLSYTYEARGE--AARFLRDRI 192
Db 123 IVIGPLYAEKTIQLCAPDGPVCCSGGN---WAAHNGYADDGMVEQAFAAGRL 173

RESULT 13
Qy Q9CDB3 PRELIMINARY; PRT; 336 AA.
AC Q9CDB3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical protein ML0099.
GS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher T., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacteux C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
DR EMBL; AL583917; CAC29607.1; --
DR Leproma; ML0099; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 336 AA; 35610 MW; 2D3B58AB526F633 CRC64;

Query Match          9.5%; Score 95; DB 16; Length 336;
Best Local Similarity 22.5%; Pred. No. 5.2;
Matches 53; Conservative 19; Mismatches 86; Indels 78; Gaps 11;

Qy 16 ACDAALIFARGSTEPG-----NMGTIVGPALANGLSHIRNIWIOGV 58
Db 71 SCPDVQLLVVPGTWESSLQDNPLDPVPDALLRNSTMTIGQFPF---SRVQTYTI--- 124

Qy 59 GGPYDAALATNPLPGTSGQANID---EGKRLFAL-----ANQKCPNTPVAGGYSQGAAL 110
Db 125 --PYTAQFHNPL--SGDKQMTYNDRAFGTRAMVQEMINVNKCPFLTLYLVGFSGQAVI 180

Qy 111 IAAAVSELS---GAVKEO-VKGVVALFGYTONLQNRGGI--PNYPRE----- 150
Db 181 AGDITSIGNGHGPDVDDLVLGVTLIADGRQGVNDIGNPDPGEGAEVTLHEVPVLGS 240
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Qy 151 -----RTKVFNCVGDVCTG-----TLIITPAHLSYTYEARGE 183
Db 241 LGMTMTGARPGGFGVLSHRTNEICAPGDLICAAPAEAFSVANPLATNLASGAGQ 296

RESULT 14
Qy Q30349 PRELIMINARY; PRT; 559 AA.
AC Q30349;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PEHR.
GS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K60;
RX MEDLINE=98052122; PubMed=9390420;
RA Allen C., Gay J., Simon-Buela L.;
RT "A regulatory locus, pehSR, controls polygalacturonase production and
RT other virulence functions in Ralstonia solanacearum.";
RL Mol. Plant Microbe Interact. 10:1054-1064(1997).
CC -1- SIMILARITY: CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING
CC DOMAIN.
DR EMBL; AF001171; AAC24599.1; --
DR HSP; P41789; INTR.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR002197; HTH_Fis.
DR InterPro; IPR001789; Response_reg.
DR InterPro; IPR002078; Sig54_interact.
DR Pfam; PF02954; HTH_8; 1.
DR Pfam; PF00072; response_reg; 1.
DR Pfam; PF00158; Sigma54_activat; 1.
DR PRINTS; PR01590; HTHFIS.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00448; REC; 1.
DR TIGRfams; TIGR01199; HTH_fis; 1.
DR PROSITE; PS00676; SIGMA54_INTERACT_2; UNKNOWN_1.
DR PROSITE; PS00045; SIGMA54_INTERACT_4; 1.
KW ATP-binding; DNA-binding; Phosphorylation; Sensory transduction;
KW Transcription regulation.
SQ SEQUENCE 559 AA; 60070 MW; 531BD5E392B558F9 CRC64;

Query Match          9.2%; Score 91.5; DB 2; Length 559;
Best Local Similarity 26.4%; Pred. No. 19;
Matches 55; Conservative 26; Mismatches 88; Indels 39; Gaps 11;

Qy 11 SGSNACPDAILIFARGSTEPGNMGITVG--PALANGLE-SHIRNIWIOGV----- 59
Db 75 SATADRTPVAV-ITAYGSAENAVEALKAGAFDYIAKPLSLDLRLSLVNLALGROQRDPDP 133

Qy 60 GPYDAALATNPLPGTSGQANIDEGKRLFALANQKCPNTPVAGGYSQGAALIAAAVSELS 119
Db 134 GSADLAERTNALLPGHSAAMQEVRSLLRLARSMAF--VVISGSGSGKERAARAHALS 191

Qy 120 -----GAVKEOVKGVALFGYTONLQNRGGIPNYPRTKVFNCVGDVCTGTL 167
Db 192 ARSPRPFVAVNCGAIPENLMEAEFFGV-----KGAFGTGADSDRQGF-----QAAHGTL 242

Qy 168 IITP-AHLSYTYEARGEAARFLRD-RIR 193
Db 243 MLDEVADLPITMQVK--LLRLQDGRVR 268

RESULT 15
Qy Q8TYQ4 PRELIMINARY; PRT; 455 AA.
AC Q8TYQ4;
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Search completed: January 2, 2003, 15:06:17  
Job time : 32 secs

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